



Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGfR	IR	IGfR/IR	IR/IGfR
R40-3-40B2-IR	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R40-4-40B12-IR	IRDMHYVWQDRDRYINGVRQWYISDRYNPGSAFYRWFID	40.3	9.0	2.0	4.5	0.2
R40-4-40G11-IR	RMGLQALAHYRKSACPIFLSSGSVIKSGEGDPFYAMFRLQ	60.4	12.9	2.0	6.5	0.2
	MPVSLFRRVWDYRDGEHETLSEHYVVPQALDRLFYSWFS	52.6	37.5	2.0	18.8	0.1

Figure 1A

Clone
 Design
 R40-3-D5-IGFR
 R40-3-A6-IGFR
 R40-X-R35-IGFR

Sequence
 XX
 PLYGGIHLIYPGTMGVPGFPRQVKVLGDADKNEYDWM
 YRGMVLGRI SDGAGK VASEPPARIGOKVFAVNFYDMFV
 SGCRLGLRWMFIVI VGS GALVCQSA SAGFYDMFV

Ratios over Background				Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
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Figure 1B

Clone Design	Sequence XXXXXXXXXXXXXXXXXXXX	Ratios over Background				Comparisons	
		E-Tag	IGFSR	IR	IGFIR/IR	IR/IGFR	
R20α-3-20D3-IR	IGGCGQHDDGNFYDWFVEALA	46.3	36.2	7.0	5.2	0.2	
R20α-3-20F1-IR	VFWNCRSQQLDFYEWFEQAA	49.0	26.0	2.8	9.3	0.1	
R20α-3-20H1-IR	RVAGAISAPGLVSNKQDGLFYSWFRE	45.6	35.3	3.3	10.7	0.1	
R20α-3-20D1-IR	VLOARHGCDVSDFYEWFA	50.8	37.5	3.0	12.5	0.1	
R20β-4-B12-IR	GAFYRWFHEALVGSERVDPV	41.9	2.9	5.7	0.5	2.0	
R20β-4-H3-IR	HEAFYDWFSAALVDGYYELMG	13.9	5.8	2.4	2.4	0.4	
R20β-4-D10-2-IR	RIGGWARSSEGFYEMFVREL	21.5	7.3	2.9	2.5	0.4	
R20β-4-C8-IR	LPAGGA?GFA?RGFYEMFES	44.9	31.1	9.6	3.2	0.3	
R20β-4-E7-IR	GHSWALVRHVDRLFYEMFDL	45.0	18.8	5.9	3.2	0.3	
R20β-4-E7-2-IR	LGTSAGCGVGHRAFYQWFQS	45.0	18.8	5.9	3.2	0.3	
R20β-4-G3-IR	RGGTFYEMFESALRKHGAG	38.6	7.5	2.0	3.8	0.3	
R20β-4-H6-IR	NSSGOQVVGLTFYSWFASQV	14.8	7.6	2.0	3.8	0.3	
R20β-4-G11-IR	FYGMFSRQLSLTPRDWGLP	39.4	7.5	1.9	3.9	0.3	
R20β-4-G8-IR	RMFYEMFWSQMGAGPTEGSA	41.2	15.1	3.4	4.4	0.2	
R20β-4-H9-IR	IGGCGQHDDGNFYDWFVEALA	43.1	8.8	2.0	4.4	0.2	
R20β-4-H8-IR	RDKPTDQEEQNMSFYEMFRH	47.9	43.7	9.3	4.7	0.2	
R20β-4-B8-IR	WSALLSVMDTGFYAMFDDAV	44.0	40.1	8.4	4.8	0.2	
R20β-4-E2-IR	SRDQTNFTFNSAGFYGMFER	16.3	13.9	2.4	5.8	0.2	
R20β-4-F4-IR	GVGTLTMSSDAFYTWV	15.3	5.9	1.0	5.9	0.2	
R20β-4-A8-IR	IGGSFVEFYGMFNDQV	43.3	36.0	6.0	6.0	0.2	
R20β-4-C4-IR	DIGSDGHGRWDSFYRMFEM	17.3	26.8	4.3	6.2	0.2	
R20β-4-D7-IR	VLOARHGCDVSDFYEMFA	44.8	36.2	5.6	6.5	0.2	
R20β-4-D2-IR	DPERMQSDVGFYEMFRAAVG	31.2	29.4	2.9	10.1	0.1	

Figure 1C





Clone
Design
R20-4-B9-IGFR
R20-4-F8-IGFR
R20-4-G12-IGFR
R20-4-D10-IGFR

Sequence
XXXXXXXXXXXXXXXXXXXX
DPERMQSDVGFYEMFRAAVG
DIGSDGHRWDSFYRWPEM
PFYQWFLDQSVGSRGGGLR
AVAPLSVRGRDSGFYSWFSS

Ratios over Background				Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
--	--	--	--	--	--
40.1	16.6	--	--	--	--
39.2	13.9	--	--	--	--
36.7	8.0	--	--	--	--
40.2	4.1	--	--	--	--

Figure 1D



Clone	Design	Sequence
A6S-3-E12-IR	XXXXXXXNFXFDMFVXXXX	GRVDWLQNRNANFYDMFVAELG
A6S-2-C1-IR		RMVFSTGAPQNFYDMFVQEMD
A6S-1-A7-IR		IHTQGLQVQRNFYDMFVNELR
A6S-2-C8-IR		MHRMÖHDGTSNFYDMFVLQWA
A6S-3-E10-IR		AMHVVAÖGGPNFYDMFVRELRL
A6S-2-D5-IR		AIÖMNGNLAFNFYDMFVRELTL
A6S-1-B2-IR		TDRKSVOEPRNFYDMFVMAAR
A6S-1-A4-IR		PHGHRGFAQSNFYDMFVTQEE
A6S-4-G3-IR		RLASASVPGQNFYDMFVDQLL
A6S-4-H8-IR		RÖSEFSTLNSNFYDMFVRELE
A6S-3-E11-IR		GQAQLSIRDVNFYDMFVQQLV
A6S-1-A1-IR		MSEPAVGVCNFXFDMFVAQLF
A6S-2-C9-IR		VGTGRARLDRNFYDMFVQÖYS
A6S-2-C4-IR		SREAVQKRANFYDMFVQÖLS
A6S-4-H10-IR		LAQFAGSRNÖNFYDMFVEQLG
A6S-4-G7-IR		GQEYFDQMGILNFYDMFVRELD
A6S-4-H2-IR		RÖPSQPPHGSNFYDMFVEAIN
A6S-2-C3-IR		LMQSLGSGSTNFYDMFVQÖMV
A6S-2-C11-IR		DQÖRSACDGTNFYDMFVCQLS
A6S-3-F3-IR		LDGTRACORVNFYDMFVCQTE
A6S-3-E5-IR		PEARRTVHSNFYDMFVAQLS
A6S-1-B7-IR		PWMLSVGIQDNFYDMFVGLDS
A6S-3-E7-IR		ASHÖRGSSDNFYDMFVAQMR
A6S-4-G6-IR		TLEREGEFGSNFYDMFVEQÖLH
A6S-2-C2-IR		DRÖSIGSVHGDFYDMFVSALG
A6S-3-F1-IR		DWDKLGSLSENFYDMFVDQLA
A6S-2-C5-IR		VRVVLNÖSGRNFYDMFVIOLE
A6S-3-E4-IR		MASWQSRTPDNFYDMFVRELRLS

Ratios over Background			Comparisons	
E-Tag	IGFSR	IR	IGFIR/IR	IR/IGFIR
--	--	--	--	--
26.2	1.3	8.0	0.2	6.2
41.2	1.3	7.0	0.2	5.4
47.2	2.3	11.1	0.2	4.8
44.9	1.5	5.5	0.3	3.7
46.9	1.6	5.0	0.3	3.1
31.9	1.2	3.7	0.3	3.1
31.6	1.8	5.3	0.3	2.9
43.3	3.6	9.2	0.4	2.6
31.3	2.3	5.1	0.5	2.2
11.5	1.7	3.6	0.5	2.1
26.3	2.3	4.4	0.5	1.9
36.9	3.7	6.5	0.6	1.8
43.6	1.3	2.3	0.6	1.8
34.5	5.6	9.6	0.6	1.7
39.2	4.4	6.9	0.6	1.6
19.1	1.4	2.2	0.6	1.6
25.5	2.6	3.9	0.7	1.5
31.1	1.6	2.4	0.7	1.5
20.9	3.3	4.6	0.7	1.4
37.1	3.0	4.2	0.7	1.4
31.6	2.5	3.5	0.7	1.4
49.2	1.6	2.3	0.7	1.4
37.2	5.0	6.3	0.8	1.3
16.8	3.1	4.0	0.8	1.3
29.7	2.4	3.1	0.8	1.3
29.7	2.3	3.0	0.8	1.3
42.9	6.1	7.0	0.9	1.1
20.9	2.1	2.3	0.9	1.1

Figure 1E



Clone D sign	Sequence	Ratios over Background		Comparisons	
		E-Tag	ICFIR	IR	ICFIR/IR
A6S-3-E9-IR	XXXXXXXXXXXXNFYDMFVXXXXX	36.6	9.0	8.9	1.0
A6S-3-E1-IR	TTCHPRGEDCNFYDMFVLQLR	36.7	6.8	6.9	1.0
A6S-4-H12-IR	VRGNDSVLIRANFYDMFVDQLS	46.3	6.1	5.8	1.1
A6S-2-D3-IR	T'PRSQVRSDHNFYDMFVYQLA	37.0	5.3	5.1	1.0
A6S-3-E8-IR	ESLTGSRPDNRNFYDMFVQTS	42.7	5.2	5.1	1.0
A6S-1-A12-IR	PQSLTEVRTGNFYDMFVVQLH	39.7	2.1	2.1	1.0
A6S-4-H3-IR	DVGMRVKETNFYDMFVRQLI	18.6	3.1	2.9	1.1
A6S-3-F7-IR	GADDIRSLNTNFYDMFVNQLS	46.2	2.3	2.1	1.1
A6S-2-D8-IR	GVSIOAGYKTNFYDMFVEAVR	31.2	2.0	1.7	1.2
A6S-3-F10-IR	VGEHRQMSVGNFYDMFVMQIA	39.0	5.9	4.5	1.3
A6S-2-D2-IR	GSSLGRSGPCNFYDMFVDQLE	44.8	4.3	3.3	1.3
A6S-4-G8-IR	HRQODVVRQGNFYDMFVQALE	33.5	3.6	2.7	1.3
A6S-4-H6-IR	QDTFLTAREGNFYDMFIRALE	11.1	2.5	1.9	1.3
A6S-2-D10-IR	EAIMREEQANFYDMFVRQLE	22.4	2.4	1.9	1.3
A6S-3-F4-IR	VCDVSTGGTNFYDMFVCQVG	41.3	2.1	1.7	1.2
A6S-4-G9-IR	PQPRASSTPLNFYDMFVQATG	37.0	13.5	9.9	1.4
A6S-3-F5-IR	GVSRRSGGDPNFYDMFVMQLR	36.2	11.8	7.8	1.5
A6S-4-H1-IR	ERFALEVOGSNFYDMFVEQVI	48.1	7.2	4.8	1.5
A6S-3-F6-IR	NLKSSATVGCNFYDMFVEQOL	18.3	3.6	2.6	1.4
A6S-2-C6-IR	MEGPPAGCPPLNFYDMFVAQVD	18.7	2.9	1.9	1.5
A6S-4-G4-IR	RLDVAGHRGGNFYDMFVKQLH	33.8	2.0	1.4	1.4
A6S-2-D7-IR	PMSDHEALNQNFYDMFVSQVL	46.7	19.2	12.1	1.6
A6S-4-G12-IR	EDRLNGGESTNFYDMFVRQLA	36.9	18.2	10.7	1.7
A6S-2-D7-IR	GKLVASTLDNPFYDMFVRQLS	32.8	12.8	7.9	1.6
A6S-4-G10-IR	SGPVVOTONGNFYDMFVHQLR	33.2	12.0	7.1	1.7
A6S-3-F9-IR	VDRAGPAGSDNFYDMFVAQLD	33.9	10.8	6.8	1.6
A6S-3-F2-IR	SLGRNDRPDENFYDMFVSQVQ	44.3	9.6	5.7	1.7
	RVMATANAPMNFYDMFVVQLQ	23.2	4.3	2.5	1.7

Figure 1E (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGF _{SR}	IR	IGF _R /IR	IR/IGF _R
A6S-4-G1-IR	XXXXXXXXXXXXNFYDWFVXXXXX	--	--	--	--	--
A6S-1-A3-IR	NGVERAGTGDNFYDWFVAQLH	36.2	31.8	15.7	2.0	0.5
A6S-3-F12-IR	PFAGKGDKTGNFYDWFVSLTG	39.9	12.6	6.0	2.1	0.5
A6S-4-G2-IR	GMPQEYMDQVNFYDWFVAQVD	41.4	7.4	4.0	1.9	0.5
A6S-1-B1-IR	MGTPAVGDGANFYDWFVRQLG	26.7	7.0	3.5	2.0	0.5
A6S-2-D11-IR	SKCKAWYGANNFYDWFVWQVD	30.6	3.7	1.9	1.9	0.5
A6S-2-D1-IR	EAASLGSODRNFYDWFVRQVV	48.4	37.4	13.5	2.8	0.4
A6S-3-E2-IR	VERSASSQDGNFYDWFVVOIR	37.8	30.6	12.0	2.6	0.4
	TSEVQRRSQDNFYDWFVAQVA	33.1	24.7	9.8	2.5	0.4

Figure 1E (Con't)





Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGfSR	IR	IGfR/IR	IR/IGfR
A6S-4-E4-IGFR	XXXXXXXXXXNFYDMFVXXXXX	--	--	--	--	--
A6S-2-D2-IGFR	ERSAAGFREGNFYDMFVAQVN	27	32	--	--	--
A6S-2-F2-IGFR	RAERGSMDRSNFYDMFVQQLP	36	30	--	--	--
A6S-4-F3-IGFR	LAMSVASRPANFYDMFVAQIV	35	30	--	--	--
A6S-4-G4-IGFR	HNSSSPMRTGNFYDMFVQELR	26	30	--	--	--
A6S-4-G3-IGFR	SALSGVPQPINFYDMFVTGM	26	30	--	--	--
A6S-2-H2-IGFR	GAAQAIREIHNFYDMFVAQVT	21	29	--	--	--
A6S-2-E3-IGFR	RGQRESDSGTNFYDMFVGAIR	40	28	--	--	--
A6S-4-C6-IGFR	VQEGLSGMEGNFYDMFVDQLF	36	28	--	--	--
A6S-4-F5-IGFR	RLDRSSTSGVNFYDMFVAQVG	25	28	--	--	--
A6S-4-H3-IGFR	GSQHSGREPHNFYDMFVAQVG	24	28	--	--	--
A6S-4-H4-IGFR	GRGDQRHETTINFYDMFVRELQ	20	28	--	--	--
A6S-2-H1-IGFR	PRMVEKPSEDNFYDMFVTQLS	20	28	--	--	--
A6S-4-E6-IGFR	RVGIQVDPHTNFYDMFVIQLT	42	27	--	--	--
A6S-4-B6-IGFR	RSSGGLLSQGNFYDMFVSQLE	24	26	--	--	--
A6S-4-D2-IGFR	SDARQAGLQENFYDMFVSQVR	23	26	--	--	--
A6S-4-G5-IGFR	PYRRSSRLGENFYDMFVMQVR	19	26	--	--	--
A6S-2-A3-IGFR	QEVTRTRDDKNFYDMFVSQIF	18	26	--	--	--
A6S-4-E2-IGFR	SRAPYGSTAGNFYDMFVQAVS	37	25	--	--	--
A6S-4-G6-IGFR	?DGQSVSSKGNFYDMFVREVA	25	25	--	--	--
A6S-4-D6-IGFR	RLMGGLAEPPNFYDMFVQDVV	20	25	--	--	--
A6S-4-F4-IGFR	SAGHHMPRESNFYDMFVKQVS	25	24	--	--	--
A6S-4-H5-IGFR	LGAETWDGINFYDMFVLMQVS	22	24	--	--	--
A6S-4-H6-IGFR	VGHSGVPPYPNFYDMFVQVVS	22	24	--	--	--
A6S-4-F6-IGFR	HHSPPGNEHGYNFYDMFVLQVA	21	24	--	--	--
A6S-3-H1-IGFR	GSIAQLIMRANFYDMFVEQTN	19	24	--	--	--
	LKSSSQPLSVNFYDMFVQOIK	18	24	--	--	--
	PASNKNSLAENFYDMFVQQTR	17	24	--	--	--
		30	23	--	--	--

Figure 1F



Ratios over Background				
Clone	Sequence	Comparisons		
Design	XXXXXXXXXXNFYDMFVXXXXX	E-Tag	IGFSR	IR IGFR/IR IR/IGFR
A6S-4-A6-IGFR	HVEHMAVGDCNFYDMFVQQLR	--	--	--
A6S-4-E3-IGFR	RCMTGMVGRGNFYDMFVGQLR	21	23	--
A6S-4-D3-IGFR	GLRSEQGNRLNFYDMFVAQIA	21	23	--
A6S-3-E10-IGFR	RVREKLPRPENFYDMFVNQIH	20	23	--
A6S-4-D1-IGFR	SNPSRQDASVNFYDMFVREVA	23	22	--
A6S-4-B2-IGFR	QSVDSLSPDSNFYDMFVEVLS	22	22	--
A6S-4-A2-IGFR	IGGQGHQDGNFYDMFVEALA	21	22	--
A6S-4-A5-IGFR	VEVQRHIRKDNFYDMFVKQID	20	22	--
A6S-4-C1-IGFR	CWABPCGDAANFYDMFVQOAS	19	22	--
A6S-4-B1-IGFR	RHERGKEGPGNFYDMFVSQV	16	22	--
A6S-4-B4-IGFR	ERSPRPALASNFYDMFVQOQV	19	21	--
A6S-4-D4-IGFR	IARMRETFQPNFYDMFVDQLA	19	21	--
A6S-3-F8-IGFR	GRGQGLKRPDNFYDMFVAQAK	18	21	--
A6S-3-H9-IGFR	YSIEVQDWNENFYDMFVSQLG	25	20	--
A6S-3-G2-IGFR	TWMWEERKQDNFYDMFVGQLK	23	20	--
A6S-4-H2-IGFR	VTFTSAVFHENFYDMFVRQVS	21	20	--
A6S-4-A3-IGFR	LAINDLVTHKNFYDMFVDQLR	19	20	--
A6S-3-G10-IGFR	GAVGLAEAGPNFYDMFVSQVQ	18	20	--
A6S-3-E5-IGFR	RYRGERHDGRNFYDMFVEQVN	24	19	--
A6S-3-H2-IGFR	QGAEGRLSEGNFYDMFVQAVS	21	19	--
A6S-3-G3-IGFR	PRLHMGSDMGDFYDMFVQVIA	21	19	--
A6S-4-H1-IGFR	IVAGARHSEVNFYDMFVIQVR	21	18	--
A6S-4-G1-IGFR	AELVGAGVRGNFYDMFVDQLV	18	18	--
A6S-4-A1-IGFR	DSSRLMLGERNFYDMFVAQIS	16	16	--
A6S-2-F1-IGFR	VGQVGRYVRSNFYDMFVQOAM	17	12	--
A6S-2-G1-IGFR	RPQLVESGSKNFYDMFVQVVR	30	8	--
A6S-1-C5-IGFR	RIHNQTERGCGNFYDMFVHQLV	30	8	--
A6S-2-B2-IGFR	EMYGDTSERVNFYDMFVSALQ	27	7	--
		30	5	--

Figure 1F (Con't)

Ratios over Background

Clone

Design

A6S-1-D5-IGFR
A6S-1-A2-IGFR
A6S-3-E6-IGFR
A6S-1-G3-IGFR
A6S-3-G4-IGFR
A6S-3-H8-IGFR
A6S-3-E3-IGFR
A6S-3-D9-IGFR
A6S-2-A1-IGFR
A6S-1-H4-IGFR
A6S-3-C1-IGFR
A6S-3-B10-IGFR

Sequence

XXXXXXXXXXNFYDWFVXXXXX
RVSGMEDLGNFYDWFVRQAQ
KDPVTVSQQGNFYDWFVQIQ
DARDHGVMVMSNFYDWFVAQVS
VATVHVGGGMNFYDWFVAQVG
CADPGACSSLNFYDWFVQMRG
NPTSVQQYGVNFYDWFVNVL
RPSLPEVRPGNFYDWFVQSVR
SLQGADFQQGNFYDWFVSELA
LSSRGVTRNFYDWFVAQVV
HKSMTTMSPLNFYDWFVAQVE
RPVIGGGGTRNFYDWFVAQMI
YDQDPPYWGILNFYDWFVREVA

Comparisons

E-Tag

IGFSR

IR

IGFR/IR

IR/IGFR

--	--	--	--
25	5	--	--
20	5	--	--
20	5	--	--
19	5	--	--
21	4	--	--
20	4	--	--
19	4	--	--
17	4	--	--
31	3	--	--
18	3	--	--
17	3	--	--
16	3	--	--



Figure 1F (Con't)

Clone	Parental/Design	Sequence	Ratios over Background		Comparisons		
			E-Tag	IGFSR	IR	IGF/IR	IR/IGF
A6L-3-D1-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDMFV	19.0	4.0	--	--	--
A6L-4-H7-IR		QRCMLVRGRISHGAGKIAYEPDCLGQKACAVNFYDMFV	22.6	19.8	26.5	0.7	1.3
A6L-4-H4-IR		QRCMLLGRISDDAGKVASEPSARRGQKVFAFNFYDMFV	37.5	3.5	4.2	0.8	1.2
A6L-4-E4-IR		YRGILVLRGRISEGAGKVASEPPARIGQKVFAFNFYDMFV	38.5	21.1	25.8	0.8	1.2
A6L-4-G7-IR		QRCMLALGRISDGAGKVASEPPARIGQKVFAFNFYDMFV	38.1	5.4	6.0	0.9	1.1
A6L-3-C3-IR		FRGRVLVGHFSDGAGKVSEPPARIGQKVFDVNFYDMFV	38.6	16.2	18.5	0.9	1.1
A6L-3-B6-IR		YRGMLVLGRISDGAGKVASEPPARIGQEVFALNFYDMFV	34.7	21.8	23.1	0.9	1.1
A6L-4-G11-IR		YRGMLVLGRISDGAGEVASEPPARIGQKVFAVNFYDMFV	33.1	27.8	30.3	0.9	1.1
A6L-4-G12-IR		VPWYAGSSSDGAGKVASEPPARIDQKVFAVNFYDMFV	27.6	2.0	2.0	1.0	1.0
A6L-3-A10-IR		YRGQLVLRGRISYAGAGVGCDDPARIGQKDFAVNFYDMFV	32.0	2.3	2.3	1.0	1.0
A6L-4-E12-IR		QRCMLVLGRISDGAGVASEPPARIGQKVCAVNFYDMFV	21.1	2.4	2.4	1.0	1.0
A6L-4-G8-IR		QRCMLVLGRISDGAGKVASELPRIQKDFAVNFYDMFV	3.1	2.4	2.4	1.0	1.0
A6L-3-C12-IR		QRCMLVLGRISDGAGKVAYEAPARIGQTFEAVNFYDMFV	30.1	3.8	3.8	1.0	1.0
A6L-4-H11-IR		QRCMLVLGRISDGAGKVASEPPARIGQEVFAVNFYDMFV	37.9	4.7	4.7	1.0	1.0
A6L-4-F10-IR		QRCMLVLGRISDGAGKVASEPPARIGQVLAVNFYDMFV	29.5	5.7	5.7	1.0	1.0
A6L-4-E9-IR		QRCMLVLGRISDGAGKVASEPPARIGQVLAVNFYDMFV	35.4	9.6	9.6	1.0	1.0
A6L-4-H8-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDMFV	31.6	10.5	10.5	1.0	1.0
A6L-3-A11-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDMFV	39.8	12.9	12.9	1.0	1.0
A6L-4-F9-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDMFV	38.2	14.6	14.6	1.0	1.0
A6L-4-G2-IR		YSGYAGSGSFDGAGKVASEPPARISQEVLAJNFYDMFV	29.0	17.5	17.5	1.0	1.0
A6L-4-E8-IR		YRGMLVLGRISDGAGKVASEPPARIGQKSAVNFYDMFV	35.7	18.4	18.4	1.0	1.0
A6L-4-H10-IR		YHGKLDLGRISVGAGKVASEPPARIGQKVFAJNFYDMFV	29.5	21.4	20.7	1.0	1.0
A6L-4-G9-IR		YRGQAGSGVSLTVAGKVASEPPARIGQKVFAJNFYDMFV	28.7	21.6	21.6	1.0	1.0
A6L-4-F7-IR		HRGMLVLGRISSEGAGNVDEPPARIGQNVFAGNFYDMFV	30.0	22.1	22.1	1.0	1.0
A6L-4-E11-IR		QRCMPVLGRISDGAGKVSEPPARIAKVFVNFYDMFI	37.1	22.6	22.6	1.0	1.0
		QCGGLVTGRISDGAGKVASEPPGGIGQKVFAJNFYDMFV	28.6	23.6	24.4	1.0	1.0
		YPMWYGSSTYLDGAGKVASEPPARIDQVFAJNFYDMFV	38.4	26.5	26.5	1.0	1.0

Figure 1G





Clone Parental/Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFIR	IR	IGFIR/IR IR/IGFIR
A6L-4-H9-IR	YRGMVLGRISDGAGKVASEPPARIGQKVFVNFYDWFV	19.0	.4.0	--	--
A6L-4-E1-IR	YRAMVLRRISDVAGIVDSEPTIRIGQKVFAGNFYDWFV	37.5	27.3	27.3	1.0 1.0
A6L-3-A5-IR	YRCMLVLGRISQAGNVASEPSSRIGQKVFAGNFYDWFV	35.4	32.6	31.4	1.0 1.0
A6L-4-G4-IR	YRCMLVLGRISDGAGKVDEPPARIGQKVFAGNFYDWFV	38.3	34.6	35.5	1.0 1.0
A6L-4-H2-IR	YRCMLGLGISAGAGIVASEPPARVQKVFAGNFYDWFV	30.4	17.7	15.2	1.2 0.9
A6L-4-E6-IR	YRCILFQGRIPDGAGKVASEPPTRIGERVFAVNFYDWFV	36.1	4.2	3.6	1.1 0.9
A6L-4-H5-IR	QCGMPVLGRISDGAGKVAFEPPARIGQKVFAGNFYDWFV	28.6	24.1	22.7	1.1 0.9
A6L-4-H3-IR	YRCMLVLGRISQAGKVASEPPARIGQKVFAGNFYDWFV	37.2	24.6	23.1	1.1 0.9
A6L-4-E5-IR	QRCMLVLGVSDGAGKVASDPASIGQNVFAVNFYDWFV	37.1	9.1	7.2	1.3 0.8
A6L-3-C5-IR	YRCMLILDRISDGASKVSEPPASIGQKVFVNFYDWFV	42.1	30.6	24.4	1.3 0.8
A6L-4-G6-IR	YRCMLVLDRISDGAGKVASEQPARIGQEVYAVNFYDWFV	42.2	21.9	17.5	1.2 0.8
A6L-3-D4-IR	YRCMLDLGRISGGVGKVAESPARIQKVVAVNFYDWFV	29.8	4.3	2.8	1.5 0.7
A6L-3-A7-IR	QRCGMVLGRISDGAGEVASEKVFVNFYDWFV	39.9	12.4	8.4	1.5 0.7
A6L-3-A6-IR	QRCMLVLGRVSDGAGKVDSAPPARIGQKVFAGNFYDWFV	31.0	21.2	14.0	1.5 0.7
A6L-4-E7-IR	QRCMLVLGRMSDGAGKVAFEPPARIGQGFAGNFYDWFV	25.5	12.3	8.8	1.4 0.7
A6L-3-C6-IR	QRCGLVLGRISDGAGKVAEPPARIGQKVFALNFYDWFV	38.4	12.5	7.1	1.7 0.6
A6L-4-F5-IR	QRCMLVLDRISDGAGKVAEPPARIGQKVFVNFYDWFV	28.8	10.9	6.7	1.6 0.6
A6L-3-B7-IR	QRCMLVLGRISDGAGEVASEPPARIGQKVFVNFYDWFV	33.8	6.3	4.1	1.5 0.6
A6L-4-F4-IR	QRCILVRGRISDGAGKVSEPPARSGEKVFVNFYDWFV	27.6	9.4	5.0	1.9 0.5
A6L-4-E3-IR	QRCMLVLGRISDGSGKVAEPPARISQKVFVNFYDWFV	38.9	17.6	9.4	1.9 0.5
A6L-0-E6-IR	YRCMLVLGRISDGDKVASEPPARIGQVFVNFYDWFV	38.0	6.9	3.8	1.8 0.5
A6L-0-E4-IR	YRCMLVLGRISDGAGHVAEPPARIGRKVFVNFYDWFV	31.0	31.0	1.8	17.0 0.1
A6L-0-H3-IR	YRCMLVLGRISDGAGKVAEPPARIGQKVAVNFYDWFV	26.0	16.0	1.3	13.0 0.1
	YRCMLVLGRISDGAGKVAEPPARIGQKVAVNFYDWFV	27.0	26.0	2.0	13.0 0.1

Figure 1G (Con't)



Clone
Parental/Design
A6L-4-F8-IGFR
A6L-2-G9-IGFR
A6L-4-E7-IGFR
A6L-4-G10-IGFR
A6L-2-E9-IGFR
A6L-2-D6-IGFR
A6L-3-H12-IGFR
A6L-4-A7-IGFR
A6L-4-B8-IGFR
A6L-4-G7-IGFR
A6L-2-D9-IGFR
A6L-4-F7-IGFR
A6L-4-E12-IGFR
A6L-4-H7-IGFR
A6L-4-H12-IGFR
A6L-2-A4-IGFR
A6L-3-D10-IGFR
A6L-2-F6-IGFR
A6L-2-B11-IGFR
A6L-1-B7-IGFR
A6L-1-D8-IGFR
A6L-0-A11-IGFR
A6L-3-B7-IGFR
A6L-1-G7-IGFR
A6L-1-B9-IGFR
A6L-1-C9-IGFR
A6L-0-G10-IGFR
A6L-1-G8-IGFR

Sequence	Ratios over Background		Comparisons	
	E-Tag	IGFR	IR	IGFR/IR IR/IGFR
YRGMLVLGRISDGAGKVA SEPPARI GQKVFAVNFYDWFV	19	4	--	--
YRGMMVQGRISDGAGKVASVSPRIGQKVI AVNFYDWFV	26	28	--	--
YRGRLGLGRISDVAGKVA CDP SARIGQKVL PVNFYDWFV	39	22	--	--
YRGMLVLGRISDGAGKVA SEPPARI GQKVFAVNFYDWFV	23	22	--	--
QGGMLVPGRISDGAGKVA SQPPARIGPKGFAGNFYDWFV	19	22	--	--
YRGMRVLGRISDGAGKVA SEPTHIGQKVPVNFYDWFV	38	21	--	--
YRGMLVLGRISDGAGKVA SEPPARI GQKVFAVNFYDWFV	34	21	--	--
YRGQGMVLGRISDGAGKVA SEPPRIGQKVPVNFYDWFV	24	21	--	--
YRGMLGLGRITGGAGKVA SEPPDRIGQHVFVDNFYDWFV	20	20	--	--
DGMLVLGRISDGAGKVA SEAPRIGQKVFAVNFYDWFV	20	19	--	--
YRGMRVRGRISDGAGKVA SDPRRIGQTVLDVNFYDWFV	19	19	--	--
YRGMWVLGRISYGAGKVA YEPPARMGQKGFVNFYDWFV	38	18	--	--
YRGMLVGGRIAGGAGIVASEPPRIGQKVFAVNFYDWFV	18	18	--	--
YRGMLGLGGRISDGAGKVA SEPPARNQKVFVNFYDWFV	15	13	--	--
YRGMLGLGRISAGAGKVA SGAPRIGQEDFAVNFYDWFV	14	13	--	--
YRGMLALGRISDGAGKVA SEPPRIGQNVFAVNFYDWFV	13	12	--	--
YRGMLVLGRISDGAGKVA SEPPRIGQKVLAVNFYDWFV	17	4	--	--
YPGMLVPGRISDGAGEGATDPPRIGQKVFAFNFYDWFV	16	4	--	--
YRGMLVPGRISDGAGKVA YEPPRIGQKIFA VNFYDWFV	15	4	--	--
YRGVLVLGRVSDGVGKVA SEPPAHRGQRFVGNFYDWFV	26	3	--	--
YRRMLVLGRISDGAA NVASGPPDRIGQKVFAGNFYDWFV	23	3	--	--
YRRMLALGRFSVDVTGDVASEPPAHIGQKVAVNFYDWFV	23	3	--	--
YRGMLVLRGRISDGAGKVA SEPPRARI GQKVFAVNFYDWFV	19	3	--	--
YRGMLILGRISDGAGKVA SEPPARVGDVAVNFYDWFV	9	3	--	--
YPGRLVGGRI SDGVGKVA SEPPRIGQKVFAVNFYDWFV	20	2	--	--
QRGLLVLGRIFDGAGKVA SDPPRIGQKDFADNFYDWFV	18	2	--	--
YRGMLVLGRISDGAGKVA FEP PARIGQNVFAVNFYDWFV	18	2	--	--
YRCMPVLGRISDGAG#VVASDRPARIGQKVFAVNFYDWFV	18	2	--	--
YRGRLVLGRISDGAGKVA AEP PASMDSKVFAGNFYDWFV	15	2	--	--

Figure 1H

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFSR	IR	IGFR/IR IR/IGFR
	GFREGNFYDWFVAQVT	--	--	--	--
E4Dα-1-B8-IR	GFREGQRWYWFVAQVT	40.7	1.0	12.3	0.1 12.3
E4Dα-3-E5-IR	GFREGYFYDWFVAQVT	39.6	2.0	1.5	1.3 0.8
E4Dα-1-A1-IR	GFREGDFYEMFVAQVT	48.7	44.9	31.4	1.4 0.7
E4Dα-2-D9-IR	GFREGQFYEMFVAQVT	22.9	3.3	2.4	1.4 0.7
E4Dα-1-B3-IR	GFREGTFYDWFVAQVT	41.8	38.6	26.5	1.5 0.7
E4Dα-1-A6-IR	GFREGNFYDWFVAQVT	56.3	51.2	32.6	1.6 0.6
E4Dα-1-A10-IR	GFREGAFYDWFVAQVT	48.9	42.2	26.5	1.6 0.6
E4Dα-1-A8-IR	GFREGAFYDWFVAQVT	46.9	41.5	26.2	1.6 0.6
E4Dα-1-B1-IR	GFREGKFYQWFVAQVT	44.1	31.1	19.7	1.6 0.6
E4Dα-2-C9-IR	GFREGDFYDWFVAQVT	34.0	8.1	4.8	1.7 0.6
E4Dα-1-A3-IR	GFREGTFYEMFVAQVT	45.3	40.3	22.5	1.8 0.6
E4Dα-1-A9-IR	GFREGNFYDWFVAQVT	46.9	41.0	22.5	1.8 0.5
E4Dα-3-F3-IR	GFREGQFYDWFVAQVT	37.2	14.1	8.0	1.8 0.6
E4Dα-2-D3-IR	GFREGQFYDWFVAQVT	35.1	16.3	8.7	1.9 0.5
E4Dα-2-D6-IR	GFREGGFYDWFVAQVT	33.2	5.6	2.8	2.0 0.5
E4Dα-3-F10-IR	GFREGQFYDWFVAQVT	27.8	4.5	2.3	2.0 0.5
E4Dα-2-D5-IR	GFREGYFYEMFVAQVT	43.8	23.8	11.4	2.1 0.5
E4Dα-3-F4-IR	GFREGDFYQWFVAQVT	25.9	7.6	3.7	2.1 0.5
E4Dα-3-E3-IR	GFREGSFYGMFVAQVT	34.6	4.0	1.9	2.1 0.5
E4Dα-3-F8-IR	GFREGSFYAMFVAQVT	20.9	16.0	7.4	2.2 0.5
E4Dα-2-C1-IR	GFREGQFYDWFVAQVT	43.1	11.6	5.0	2.3 0.4
E4Dα-1-B4-IR	GFREGIFYEMFVAQVT	45.3	6.6	2.9	2.3 0.4

Figure II





Clone Design	Sequence
E4D α -4-H5-IR	GFREGNEXYDWFVAQVT
E4D α -1-B12-IR	GFREGSFYEMFQAQVT
E4D α -4-G2-IR	GFREGNFYDWFVAQVT
E4D α -3-F9-IR	GFREGSFYDWFVAQVT
E4D α -4-G6-IR	GFREGDFYDWFVAQVT
E4D α -4-H9-IR	GFREGDFYQWFFVAQVT
E4D α -2-C10-IR	GFREGGFYDWFVAQVT
E4D α -1-B2-IR	GFREGDFYGMFQAQVT
E4D α -3-F12-IR	GFREGVFYDWFVAQVT
E4D α -2-D11-IR	GFREGGFYEMFQAQVT
E4D α -4-H2-IR	GFREGSFYDWFQAQVT
E4D β -4-A12-IR	GFREGNFYEMFQAQVT
E4D β -4-A10-IR	GFREGKFYDWFQAQVT
E4D β -4-E10-IR	GFREGGFYEMFVAQVT
E4D β -4-B11-IR	GFREGTFYDWFVAQVT
E4D β -4-C10-IR	GFREGGFYEMFQAQVT
E4D β -4-E8-IR	GFREGDFYEMFQAQVT
E4D β -4-G7-IR	GFREGGFYDWFVAQVT
E4D β -4-C8-IR	GFREGGFYDWFVAQVT
E4D β -4-A8-IR	GFREGGFYDWFVAQVT
E4D β -4-A9-IR	GFREGGFYDWFVAQVT
E4D β -4-G11-IR	GFREGTFYDWFQAQVT
E4D β -4-B9-IR	GFREGNFYEMFQAQVT
E4D β -4-F10-IR	GFREGSFYDWFQAQVT
E4D β -4-D12-IR	GFREGNFYDWFVAQVT
E4D β -4-B8-IR	GFREGDFYDWFVAQVT
E4D β -4-G10-IR	GFREGAFYDWFVAQVT

Ratios over Background		Comparisons	
E-Tag	IGFSR	IR	IGFSR/IR IR/IGFSR
--	--	--	--
47.2	36.0	14.7	2.4 0.4
47.6	33.4	13.8	2.4 0.4
23.4	20.4	8.6	2.4 0.4
36.2	15.6	6.3	2.5 0.4
26.0	4.9	2.0	2.5 0.4
47.8	24.8	9.5	2.6 0.4
42.4	23.2	9.0	2.6 0.4
39.4	18.7	7.2	2.6 0.4
38.9	16.6	5.6	3.0 0.3
40.2	11.1	3.3	3.4 0.3
37.8	33.9	8.2	4.1 0.2
41.1	8.3	28.7	0.3 3.5
5.8	1.2	2.4	0.5 2.0
9.6	1.2	2.2	0.5 1.8
36.1	15.2	26.9	0.6 1.8
27.8	13.3	23.7	0.6 1.8
28.7	16.7	28.2	0.6 1.7
30.9	14.7	24.7	0.6 1.7
35.5	22.5	32.9	0.7 1.5
31.2	14.5	22.2	0.7 1.5
35.8	9.0	13.1	0.7 1.5
28.9	9.7	13.6	0.7 1.4
27.2	9.1	12.5	0.7 1.4
7.7	1.5	2.1	0.7 1.4
41.1	27.2	36.1	0.8 1.3
35.9	27.0	35.2	0.8 1.3
38.5	25.5	33.7	0.8 1.3

Figure II (Con't)



E4D}-4-D9-IR
E4D}-4-F8-IR
E4D}-4-E12-IR
E4D}-4-H12-IR
E4D}-4-C9-IR
E4D}-4-H9-IR
E4D}-4-G9-IR
E4D}-4-F12-IR
E4D}-4-F9-IR
E4D}-4-F7-IR
E4D}-4-B7-IR

GFREGSFYDWFEAQVT
GFREGSFYDWFFAQVT
GFREGSFYEMFDAQVT
GFREGAFYDWFEAQVT
GFREGQFYDWFFAQVT
GFREGNFYDWFFAQVT
GFREGDFYDWFFAQVT
GFREGSFYEMFEAQVT
GFREGGFYDWFLLAQVT
GFREGGFYAWFPAQVT
GFREGGFYEMF?AQVT

34.1	19.3	25.7	0.8	1.3
39.3	35.6	44.4	0.8	1.2
40.2	27.8	33.4	0.8	1.2
41.2	27.1	32.3	0.8	1.2
38.0	22.5	27.6	0.8	1.1
38.7	33.3	36.6	0.9	1.1
10.9	4.9	5.6	1.0	1.0
14.8	5.9	6.1	1.1	0.9
39.3	31.3	28.3	1.1	0.9
31.0	22.2	19.5	1.1	0.9
--	--	--	--	--

Figure 11 (Con't)

Clone	Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGFSR	IR	IGFSR/IR	IR/IGFSR	
	E4D-2-E7-IGFR	GFREGNFYDMFVAQVT	--	--	--	--	--	--
	E4D-2-E7-IGFR	GFREGDFYDMFRAQVT	20.8	22.8	--	--	--	--
	E4D-2-C11-IGFR	GFREGSFYDMFVAQVT	21.5	22.6	--	--	--	--
	E4D-2-B1-IGFR	GFREGDFYGMFQAQVT	22.0	22.5	--	--	--	--
	E4D-2-D10-IGFR	GFREGGFYDMFQAQVT	20.6	22.1	--	--	--	--
	E4D-2-A9-IGFR	GFREGDFYDMFVAQVT	17.4	21.5	--	--	--	--
	E4D-2-E5-IGFR	GFREGDFYDMFQAQVT	24.2	21.2	--	--	--	--
	E4D-2-H9-IGFR	GFREGGFYDMFVAQVT	19.1	20.7	--	--	--	--
	E4D-1B-C4-IGFR	GFREGDFYDMFQAQVT	24.3	20.5	--	--	--	--
	E4D-2-E10-IGFR	GFREGNFYDMFQAQVT	21.0	20.5	--	--	--	--
	E4D-2-F4-IGFR	GFREGNFYDMFLAQVT	25.0	20.2	--	--	--	--
	E4D-2-C10-IGFR	GFREGHFYDMFQAQVT	22.8	20.1	--	--	--	--
	E4D-3-D8-IGFR	GFREGQFYEMFQAQVT	21.1	19.8	--	--	--	--
	E4D-3-F9-IGFR	GFREGSFYEMFQAQVT	22.6	19.7	--	--	--	--
	E4D-1B-E5-IGFR	GFREGDFYDMFLAQVT	24.2	18.8	--	--	--	--
	E4D-2-F3-IGFR	GFREGHFYDMFVAQVT	23.6	18.0	--	--	--	--
	E4D-3-D5-IGFR	GFREGQFYEMFVAQVT	22.2	18.0	--	--	--	--
	E4D-3-G10-IGFR	GFREGQFYDMFQAQVT	22.1	17.6	--	--	--	--
	E4D-2-F6-IGFR	GFREGQFYDMFVAQVT	24.6	17.5	--	--	--	--
	E4D-2-F7-IGFR	GFREGDFYQMFQAQVT	19.0	17.5	--	--	--	--
	E4D-3-B7-IGFR	GFREGNFYDMFVAQVT	23.0	16.4	--	--	--	--
	E4D-1B-C12-IGFR	GFREGSFYDMFVAQVT	23.0	16.1	--	--	--	--
	E4D-3-B1-IGFR	GFREGHFYEMFQAQVT	21.6	16.0	--	--	--	--
	E4D-2-E2-IGFR	GFREGDFYDMFSAQVT	21.9	14.1	--	--	--	--
	E4D-2-D1-IGFR	GFREGHFYDMFQAQVT	24.5	13.2	--	--	--	--
	E4D-1-D4-IGFR	GFREGYFYDMFKAQVT	18.9	12.4	--	--	--	--
	E4D-1B-A10-IGFR	GFREGHFYDMFQAQVT	23.9	10.8	--	--	--	--
	E4D-1B-A3-IGFR	GFREGDFYDMFQAQVT	22.2	10.8	--	--	--	--
	E4D-1-B5-IGFR	GFREGTFYDMFVAQVT	19.0	10.8	--	--	--	--

Figure 1J



Clone	Sequence	Ratios over Background		Comparisons	
Design		E-Tag	IGfSR	IR	IGfR/IR IR/IGfR
E4D-1B-B8-IGfR	GFREGNFYDWFVAQVT	--	--	--	--
E4D-1B-B8-IGfR	GFREGDYYGWFEAQVT	23.8	10.7	--	--
E4D-1-G7-IGfR	GFREGDFYAWFMAQVT	14.3	10.5	--	--
E4D-1B-A11-IGfR	GFREGNFYEWFLAQVT	24.0	10.0	--	--
E4D-1-C3-IGfR	GFREGSFYDWFDAQVT	15.8	9.3	--	--
E4D-2-H1-IGfR	GFREGNFYDQFVAQVT	19.6	4.9	--	--
E4D-1-C2-IGfR	GFREGHFYEWFAAQVT	11.5	4.5	--	--
E4D-1B-A12-IGfR	GFREGNFYEWFVAQVT	18.4	3.5	--	--
E4D-1B-A1-IGfR	GFREGKFYDWFVAQVT	22.5	2.9	--	--
E4D-2-A3-IGfR	GFREGMFDVQLLAQVT	22.7	2.1	--	--

Figure 1J (Con't)



Clone	Sequence
Design	XXXXXXXXFHENFYDWFVRQVSXXXXXX
Parental	VTFTSAVFHENFYDWFVRQVS
H2CA-4-F11-IR	TYKARFLHENFYDWFNRQVSQYFGRV
H2CA-4-E10-IR	QRLSLHEQFYDWFVGQVSPLGAGG
H2CA-4-G3-IR	GGGKVNPHEDFYGWFVQGFSGVSDR
H2CA-3-A11-IR	LVGDAPFHEDFYDWFARQVFGCCQEQ
H2CA-4-F8-IR	TGAEVSFHENFYDWFDRQVSSWLDR
H2CA-4-G4-IR	QPHSSRLHESFYDWFDRQVPWYALDR
H2CA-4-F4-IR	SRALAAVHEQFYDWFVRQVSGLDWGY
H2CA-4-H10-IR	QPKDGTLHENFYDWFVRQVSSSGWVG
H2CA-4-F1-IR	RGRLIQLHEDFYDWFRLQVSGMGGS
H2CA-3-D5-IR	QRGAPKSDENFYDWFVRQVLRFGEND
H2CA-4-E11-IR	AARTSLFHEDFYEWFDQRQVRQEGMWG
H2CA-3-B6-IR	GTSNHSLHENFYDWFVRQQLSSVQSSG
H2CA-3-A9-IR	VSHVHLFHENFYDWFVRQQLAAEGFSG
H2CA-4-H5-IR	GRQDSGLHENFYDWFVSRQVQGEVALG
H2CA-3-C9-IR	SNDERQFHETFYDWFVRQVSADGADR
H2CA-3-A10-IR	LSTEQRHHEKFYDWFVHQVSTSGGT
H2CA-3-A3-IR	SLSRQFHENFYDWFARQVSELEGV
H2CA-4-G8-IR	IPGRRSLHENFYDWFVRQVSPGGSA
H2CA-4-G9-IR	TQKAQSLDEKFYDWFVRQVSGGLTG
H2CA-4-G10-IR	VSQLSDFHENFYGWFPARQIAGQAEWT
H2CA-4-H7-IR	NGTSQALHQNFYDWFPAQOISGSEPGP
H2CA-4-F9-IR	VGQSVTFHGDFYDWFDRQLSGSQEFG
H2CA-4-F7-IR	TIDHPLHEQFYDWFARQVSDLES LG
H2CA-3-D10-IR	PNVGYAFHENFYDWFIRQVSIIEKAG
H2CA-3-B1-IR	SRGSGVFHESFYNMFDROVSEWIQFG
H2CA-3-A5-IR	QPVSGSVHERFYDWFVRQVSGSAGGG
H2CA-4-F10-IR	ASQLPPVYENFYEWFDQRQVSLDAQRE

E-Tag	Ratios over Background		Comparisons	
	IGFSR	IR	IGFSR/IR	IR/IGFSR
--	--	--	--	--
29.8	17.5	16.3	1.1	0.9
37.7	2.2	18.1	0.1	8.2
31.2	4.4	18.8	0.2	4.3
36.1	13.4	25.7	0.5	1.9
35.6	12.1	22.0	0.5	1.8
36.0	21.1	33.5	0.6	1.6
37.1	23.3	34.3	0.7	1.5
39.8	25.0	35.6	0.7	1.4
33.5	5.1	6.6	0.8	1.3
36.1	19.6	25.1	0.8	1.3
39.3	24.3	31.9	0.8	1.3
8.2	2.6	3.2	0.8	1.2
35.9	9.9	12.1	0.8	1.2
37.3	30.1	36.2	0.8	1.2
38.6	35.4	37.3	1.0	1.1
29.3	5.1	5.6	0.9	1.1
37.2	16.9	19.1	0.9	1.1
29.2	28.6	32.2	0.9	1.1
32.4	29.1	31.6	0.9	1.1
36.1	34.4	36.4	0.9	1.1
34.2	35.5	37.7	0.9	1.1
37.0	36.0	40.0	0.9	1.1
37.5	36.7	39.5	0.9	1.1
37.7	37.6	39.9	0.9	1.1
18.7	3.6	3.5	1.0	1.0
26.5	21.4	21.5	1.0	1.0
32.9	22.9	22.4	1.0	1.0
26.6	27.7	28.5	1.0	1.0

Figure 1K

502877.1



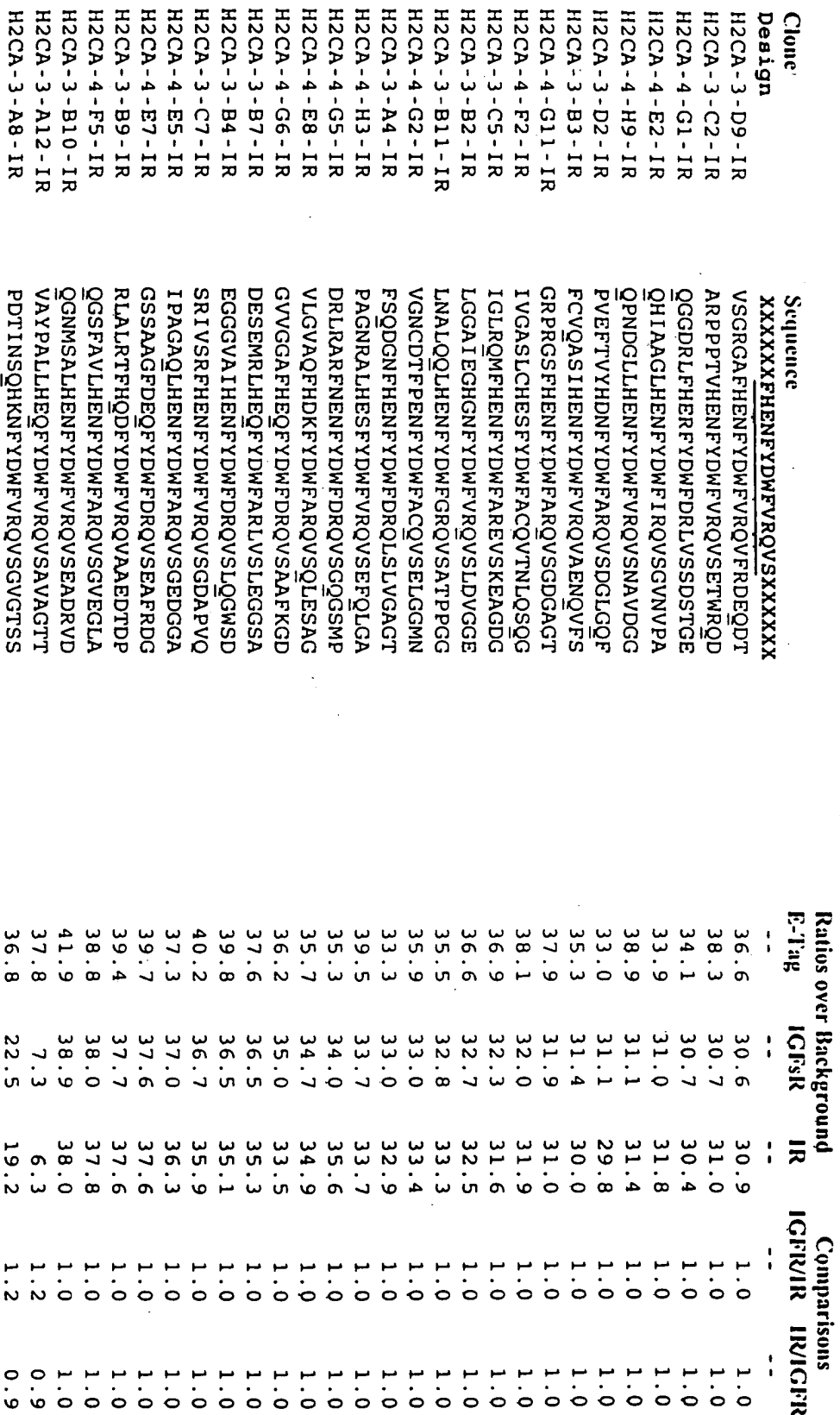


Figure 1K (Con't)



46397.1

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	ICFSK	IK	ICFR/IK	IR/ICFR
H2CA-3-D12-IR	XXXXXXXXXHEHNFYDMFVRQVSGXXXXX	--	--	--	--	--
H2CA-3-B5-IR	SEVDSDRHENFYDMFVRQVSGICLQD	36.8	34.1	29.6	1.2	0.9
H2CA-4-E1-IR	PAPADAFDHNFYDMFARQISATTTIQ	38.8	35.2	30.5	1.2	0.9
H2CA-3-D3-IR	MVQRISIHENFYDMFARQISGSAVP	29.8	12.5	11.3	1.1	0.9
H2CA-4-E3-IR	GNVRGQFHQCFYDMFARQVSGSEGA	33.1	29.9	27.5	1.1	0.9
H2CA-3-A6-IR	PDAEKQFHETFGMFWARQISEDANS	33.3	32.3	30.2	1.1	0.9
H2CA-4-E12-IR	FCRGVHCDEFYDMFVQCVSGALLG	36.0	32.4	29.4	1.1	0.9
H2CA-4-E9-IR	ETPTLTELHQCFYDMFVRQVSGFPQGV	34.0	33.1	30.6	1.1	0.9
H2CA-4-F3-IR	QHRGPHFHEDFYDMFVRQVSSAVPSD	38.8	33.7	29.7	1.1	0.9
H2CA-4-H6-IR	RODPGLFHDFYDMFRLVAMDCQE	41.0	34.2	32.0	1.1	0.9
H2CA-3-D1-IR	QAAVGVCKNDFYAMFACQVEDFAKA	37.1	34.5	30.8	1.1	0.9
H2CA-4-H2-IR	RMNLIQFHNENFYDMFDRQVSLRQCG	41.8	35.3	32.8	1.1	0.9
H2CA-3-D4-IR	RSEQYRPHENFYEMFPROVSRMGLLG	38.7	35.5	32.3	1.1	0.9
H2CA-3-C1-IR	GAGGRDFDEDFYDMFVRQVSGQVTSG	34.5	35.5	31.3	1.1	0.9
H2CA-4-H4-IR	SPEGNLVHDQFYDMFVROLSTSTAGT	39.9	36.1	32.9	1.1	0.9
H2CA-3-D8-IR	QCGGLGDFDEDFYDMFARQVRRDRAD	37.8	36.7	33.1	1.1	0.9
H2CA-4-F6-IR	LSQGVGFQENFYEMFPERQVSGMDGRD	38.5	37.0	33.7	1.1	0.9
H2CA-4-F6-IR	VFERSRCHDNFYDMFPCQVSGQADCG	38.7	37.5	35.2	1.1	0.9
H2CA-3-C11-IR	LLASRAFHENFYDMFARQVSGTQPPG	38.6	38.0	34.7	1.1	0.9
H2CA-4-E4-IR	VPDQQLFHESFYDMFVRQVSGAGCPAD	40.3	38.3	36.1	1.1	0.9
H2CA-3-C4-IR	ANQMGREFHNFYDMFDRQVRYERGT	41.9	38.4	35.0	1.1	0.9
H2CA-4-E6-IR	PSRKDGLHOSFYDMFARQVQDMGARA	39.3	38.8	35.8	1.1	0.9
H2CA-3-D7-IR	QAVTRRPHENFYDMFARQVSEEGMS	42.5	39.2	35.5	1.1	0.9
H2CA-4-G12-IR	GVAVQGVQANFYDMFVRQVSDMNSG	35.3	15.2	11.6	1.3	0.8
H2CA-3-D6-IR	GHQBDLHESFYDMFVRQVSEAECCG	37.6	19.4	15.1	1.3	0.8
H2CA-4-H12-IR	DRPSSFHNFYEMFARQVSGSSG	39.4	36.2	27.6	1.3	0.8
H2CA-3-D11-IR	ERTAEATHQCFYDMFVRQVSGMDES	40.0	38.4	29.3	1.3	0.8
H2CA-3-C12-IR	LTSQGLSHEDFYDMFVRQVSGVGINED	38.1	32.9	27.2	1.2	0.8
H2CA-3-C12-IR	PDRSDRLDNFYDMFVRQVSGVINED	38.5	38.4	31.7	1.2	0.8

Figure 1K (Cont)



Clone
Design
H2CA-4-G7-IR
H2CA-3-C6-IR
H2CA-3-B8-IR

Sequence
XXXXXXXXFHENFYDWFVRQVSXXXXXXXX
RAGVGGLHDNFYDWFVRQVSGDSDGP
ADCYVQLHENFYDWFRRQVCNLQEGM
RQGHAGFHDFYDWFVRQVSGSTPQV

Ratios over Background				Comparisons	
E-Tag	IGfSR	IR	IGfR/IR	IR/IGfR	
--	--	--	--	--	--
35.9	34.7	23.7	1.5	0.7	
38.7	37.6	28.2	1.3	0.7	
37.8	19.6	9.9	2.0	0.5	

Figure 1K (Con't)



Clone Design Parental	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR
	XXXXXXXXFHENFYDMFVRQVSXXXXXX VTFTSAVFHENFYDMFVRQVS	--	--	--	--	--
H2CA-4-G9-IGFR	GIISQSCPESFYDMFAGQVSDPWWCM	29.8	17.5	16.3	1.1	0.9
H2CA-4-H6-IGFR	VGRASGFPENFYDMFGRQLSLQSGEQ	8.6	9.5	0.6	16.0	0.1
H2CA-4-F-IGFR5	VGYOQGDENFYDMFIRQVSGRLGVQ	4.9	10.5	0.7	14.6	0.1
H2CA-4-H8-IGFR	SACQFDCHEFYDMFARQVSGCAAYG	5.5	9.7	0.8	12.3	0.1
H2CA-4-F11-IGFR	SAQQLFQESFYDMFLRQVAESSQPN	5.6	9.2	1.0	9.4	0.1
H2CA-4-F6-IGFR	AVRATRFDEAFYDMFVRQISDQGNK	3.5	6.8	1.0	6.7	0.1
H2CA-4-F10-IGFR	VNQSISIHENFYDMFERQVSHQGVN	3.9	7.3	1.1	6.4	0.2
H2CA-1-A3-IGFR	APDPSDFOEI FYDMFVRQVSRMPGGG	4.9	5.7	1.0	5.9	0.2
H2CA-3-C8-IGFR	SSCDGAGHESFYEMFVRQVSGCRSV	7.7	3.8	0.8	5.1	0.2
H2CA-2-B9-IGFR	RAGSSDFHEDFYEMFVRQVSLSLKGK	15.1	5.6	1.2	4.8	0.2
H2CA-4-H4-IGFR	QAVQPGFHBEFYDMFVRQVSTGVGGG	9.3	7.0	1.7	4.2	0.2
H2CA-4-F7-IGFR	SSIGGFHENFYDMFSLQSPPLK	3.9	4.1	1.0	4.2	0.2
H2CA-3-D6-IGFR	QSPVGSSHEDFYDMFFRQVAQSGAHQ	1.5	3.2	0.8	4.1	0.2
H2CA-3-D8-IGFR	NYRRQVFNGNFYDMFDRQVSLVTPG	8.3	9.0	2.2	4.0	0.3
H2CA-4-G11-IGFR	TLDDGSFEEQFYDMFVRQVLSYRTNPD	10.9	7.2	1.8	4.0	0.3
H2CA-4-F1-IGFR	FYVQQWGHENFYDMFDRQVSSQSGAG	10.8	9.5	2.5	3.9	0.3
H2CA-3-D7-IGFR	LRRQAPVEENFYDMFVRQVSGDRVGG	5.8	3.5	0.9	3.8	0.3
H2CA-1-A7-IGFR	RCGRELXSTFYDMFDRQVAGRTCPG	13.3	3.0	0.8	3.7	0.3
H2CA-2-B4-IGFR	CCLLCRFQONFYDMFVCQGISRLRPL	8.0	2.2	0.6	3.7	0.3
H2CA-2-B3-IGFR	PPLASDLVDQFYGMFVQQVSPPRGGG	3.5	4.1	1.1	3.6	0.3
H2CA-2-B2-IGFR	GAPVDQLHEDFYDMFVRQVSLGTDK	7.7	3.8	1.0	3.6	0.3
H2CA-3-D4-IGFR	RSASGSLPEQFYDMFVRQVSLSGTDK	4.1	3.4	1.0	3.5	0.3
H2CA-4-F2-IGFR	SRVTVFHENFYDMFVRQVSLSDAISG	17.6	13.8	4.1	3.4	0.3
H2CA-3-D11-IGFR	DERGKGFREDFYDMFVRQVSESFRGQ	9.3	12.8	4.2	3.0	0.3
H2CA-4-H9-IGFR	RGAVAGFHDQFYDMFDRQVSRVHKFG	12.2	6.9	2.3	3.0	0.3
H2CA-2-B11-IGFR	AICDAGFHEHFYDMFALQVSDCGROS	8.7	5.6	1.9	3.0	0.3
H2CA-3-E8-IGFR	LGYQEPFQONFYDMFVRQVSGAENAG	11.9	4.6	1.6	3.0	0.3
		13.2	6.3	2.2	2.9	0.3

Figure 1L

Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGfsR	IR	IGfR/IR	IR/IGfR	
H2CA-3-E6-IGFR	XXXXXXXXFHENFYDMFVRQVSGSSST	--	--	--	--	--	--
H2CA-4-F4-IGFR	WRGHGTFHEDFYDMFVRQVSGSSST	15.7	8.7	3.1	2.8	0.4	
H2CA-3-D10-IGFR	GGRVGVLFHENFYDMFDRQVSLRGADG	11.5	7.4	3.0	2.5	0.4	
H2CA-3-E1-IGFR	CNLTAGFHEQFYHMFALQVCGDAENA	9.4	6.8	2.9	2.3	0.4	
H2CA-2-B6-IGFR	ERGEDMFHENFYDMFVRQISGRQGGG	12.5	6.4	2.8	2.3	0.4	
H2CA-3-E11-IGFR	TNQGFGFYDSFYGMFVRQIQYGVDSG	18.0	6.2	2.7	2.3	0.4	
H2CA-4-H2-IGFR	HLADGQFHEKFYDMFERQISSRCNDG	4.7	2.2	1.0	2.2	0.5	
H2CA-3-C11-IGFR	QTFGKSLHENFYDMFVRQVSRREGGD	9.8	9.9	4.8	2.1	0.5	
H2CA-2-B8-IGFR	FRTLAAQHDSFYDMFDRQVSGAAGER	9.3	3.3	1.6	2.1	0.5	
	SASTHQFHENFYDMFVRQVSGAQKIL	14.6	7.9	3.9	2.0	0.5	

Figure 1L (Con't)



Clone	Sequence	Ratios over Background				Comparisons	
Design		E-Tag	IGFSR	IR	IGF/IR	IR/IGFR	
Parental	XXXXXXXXXXFXMFXXXXXX VTFTSAVFHENFYDMFVRQVS	--	--	--	--	--	--
H2CBa-3-B12-IR	QSDSGTVHDFRYGWFRTD*A	29.8	17.5	16.3	1.1	0.9	
H2CBa-3-D2-IR	WTDVDGFHSGFYRMFQNGMER	26.0	1.3	20.4	0.1	16.0	
H2CBa-3-D12-IR	VASGHLHGQFYRMFVDQFAL	20.6	1.7	12.1	0.1	7.0	
H2CBa-3-H5-IR	QARVGNVHQFYEMFREVMQ	24.6	2.1	14.0	0.1	6.7	
H2CBa-3-B6-IR	VGDFCVSHDCFYGMFLRESM	16.7	2.4	15.1	0.2	6.3	
H2CBa-3-G11-IR	SGSRPVFHEQFYEMFVDQLG	31.4	2.5	13.9	0.2	5.6	
H2CBa-3-A6-IR	QFSAGAFHGDIFYGMFRALYNG	22.7	1.4	6.4	0.2	4.7	
H2CBa-3-B1-IR	SRFDERLHHQFYEMFRVLNER	25.9	1.7	7.1	0.2	4.3	
H2CBa-3-F8-IR	DSVNSDLHRAFYGMFAEQMRA	33.4	6.0	25.5	0.2	4.3	
H2CBa-3-E11-IR	GSVDREIHGPFYSWFSEQLWG	23.0	4.8	19.8	0.2	4.1	
H2CBa-3-G4-IR	SAKTPVLHDGFYMWFEAQSES	14.0	2.2	8.5	0.3	4.0	
H2CBa-3-D3-IR	LVVGRFRHQSFYDMFVAAGG	24.9	2.2	6.9	0.3	3.2	
H2CBa-3-C1-IR	IMWPCTFQDPFYCMFQTEQGR	23.6	2.6	8.0	0.3	3.1	
H2CBa-3-C3-IR	VVGPLDIHERFYGMFHQCGA	27.0	5.6	16.4	0.3	2.9	
H2CBa-3-G3-IR	VVPKAGFHEAFYEMFRRQDRD	23.3	1.1	3.1	0.4	2.8	
H2CBa-3-E4-IR	QSFVTSVHTRFYAMFASALEM	23.7	6.7	17.6	0.4	2.6	
H2CBa-3-G5-IR	SRGLGLYHSGFYGMFERQFNQ	28.8	8.3	21.9	0.4	2.6	
H2CBa-3-B11-IR	GADTGAVHRRFYLMFEQLSGG	26.7	7.0	17.2	0.4	2.5	
H2CBa-3-A1-IR	PGNRPTFHAFFYRMFREAQGS	28.0	8.6	19.4	0.4	2.3	
H2CBa-3-H1-IR	VAVAMGLHESFYAMFENQFSD	31.3	11.3	24.9	0.5	2.2	
H2CBa-3-F12-IR	GFNTGTGFHDQFYWMFEAAGG	27.2	10.6	23.9	0.4	2.2	
H2CBa-3-H7-IR	GDGLTAFHQGFYEMFDIQMYG	21.1	6.1	12.7	0.5	2.1	
H2CBa-3-C12-IR	VGVNRQGFHTRFYAMFDEQLGG	21.0	9.7	19.1	0.5	2.0	
		26.0	12.7	24.7	0.5	1.9	

Figure 1M



Clone Design	Sequence	E-Tag		Ratios over Background		Comparisons	
	XXXXXXXXFHXFXFXMFXXXXXX	--	--	--	--	--	--
H2CBα-3-D11-IR	GPRGQRLHDAFYSWFDALRVN	27.8	13.0	24.8	0.5	1.9	
H2CBα-3-H12-IR	LGT LAVFHELFGWFERQLGCG	27.4	7.2	12.4	0.6	1.7	
H2CBα-3-A10-IR	LG YCGFNCQFYRWFDNLADR	27.1	13.2	22.3	0.6	1.7	
H2CBα-3-A5-IR	FSGWADYQSGFYQWFAEELAN	28.3	16.1	28.1	0.6	1.7	
H2CBα-3-C4-IR	WGPFVSFDES FYRWFAQASDD	30.7	17.2	29.2	0.6	1.7	
H2CBα-3-B8-IR	PRNEG LVHGLFYDWFQALSG	25.6	11.3	18.6	0.6	1.6	
H2CBα-3-H11-IR	DEGAPLDVMFYRWFEQAVRG	28.8	14.0	22.4	0.6	1.6	
H2CBα-3-E10-IR	QSGNRGSHGAFYSWFRDVLAN	27.7	14.3	23.0	0.6	1.6	
H2CBα-3-C2-IR	MRQRDGFNSFYGWFAALGE	28.4	17.0	26.7	0.6	1.6	
H2CBα-3-F6-IR	SEERKKVHSQFYSWFDRQLTG	27.3	14.5	21.8	0.7	1.5	
H2CBα-3-D4-IR	PSPNAPFHGCFYDWFWDVQGS	29.0	18.9	27.1	0.7	1.4	
H2CBα-3-A7-IR	FHRPGSFNTNFYQWFDQMNQ	29.1	19.4	26.9	0.7	1.4	
H2CBα-3-H4-IR	SDDSTLNGRFYTWFMQLD	27.2	20.1	27.9	0.7	1.4	
H2CBα-3-B7-IR	QRCGGFHGFGYSWFRSQSL	28.6	18.0	23.6	0.8	1.3	
H2CBα-3-F9-IR	SGSRPVFHEQFYEMFVDQLGL	26.1	19.1	24.3	0.8	1.3	
H2CBα-3-H6-IR	GGSSQAFHGA FYEMFSAQLRG	24.8	21.6	27.3	0.8	1.3	
H2CBα-3-F5-IR	AFVSE RVNQRFYDWF RDQMS	29.4	22.0	27.8	0.8	1.3	
H2CBα-3-A2-IR	VRHPTRFHDEFYRWFTQLTT	30.7	22.5	29.1	0.8	1.3	
H2CBα-3-F3-IR	ARLLNIFDRGFYXW FQRQLDE	16.3	6.7	9.0	0.7	1.3	
H2CBα-3-G6-IR	PSLSSNLHESFYRWFDQLVST	24.9	21.0	24.4	0.9	1.2	
H2CBα-3-G7-IR	FAFGLGFHQGFYDWF AHQLEG	24.4	18.7	23.0	0.8	1.2	
H2CBα-3-C5-IR	VSATVMLHREFYDWFGLQLLD	26.4	21.2	25.4	0.8	1.2	
H2CBα-3-G1-IR	GGVSGVLHDRFYSWFERQLAG	26.9	21.5	26.3	0.8	1.2	
H2CBα-3-E3-IR	GLGIASFHEG FYSWFTAQLGA	24.2	17.2	19.3	0.9	1.1	

Figure 1M (Con't)



Clone	Sequence	Ratios over Background				Comparisons	
Design	XXXXXXFXHXXFXMFXXXXXX	E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
H2CBα-3-A9-IR	RVDAAALNAGFYEWFRGVIQ	30.5	21.7	24.1	0.9	1.1	
H2CBα-3-C11-IR	GGAGRSFHDAFYEWFERQMAC	26.4	21.8	23.2	0.9	1.1	
H2CBα-3-B4-IR	EGARQGFHARFYSWFAOQLAL	30.9	22.0	24.3	0.9	1.1	
H2CBα-3-F11-IR	VLLPGVVHGGFYDWFSCRQLSS	24.5	22.5	23.9	0.9	1.1	
H2CBα-3-G10-IR	GALSDRYNNVFYDWFREQLLG	28.3	23.6	27.1	0.9	1.1	
H2CBα-3-D7-IR	PDSFMSLHQRFYSWFOAQVGT	31.4	23.6	25.3	0.9	1.1	
H2CBα-3-E2-IR	RVYKANFNHNEFYGWFREQLLG	26.8	24.0	25.7	0.9	1.1	
H2CBα-3-B5-IR	HSGMRDVHARFYSWFSEQLSG	28.7	25.0	26.4	0.9	1.1	
H2CBα-3-C7-IR	ARLLERFQDPFYEWFEETLMD	30.0	25.2	28.7	0.9	1.1	
H2CBα-3-G9-IR	RNSSGNFHDKFYNWFEAQLKG	27.8	25.2	26.7	0.9	1.1	
H2CBα-3-A12-IR	GSMSPVFENDQFYGWFRLVDE	28.0	26.4	28.7	0.9	1.1	
H2CBα-3-C9-IR	SCTGRQFDGCFYAMFEDQLVG	32.1	28.7	31.9	0.9	1.1	
H2CBα-3-B10-IR	GIAVQSLHDSFYRWFEDNALGS	33.5	30.8	33.2	0.9	1.1	
H2CBα-3-E1-IR	IGPPGSLHRGFYDWFABQVEA	31.7	30.5	29.0	1.1	1.0	
H2CBα-3-G12-IR	GAAGISFHRGFYDWFQAQVRD	29.1	31.4	29.8	1.1	1.0	
H2CBα-3-F7-IR	GVDVTFHKDFYSWFOQLNG	23.2	20.7	20.3	1.0	1.0	
H2CBα-3-G8-IR	WAGRAGIHGGFYEWFNKQLRG	22.8	20.9	20.4	1.0	1.0	
H2CBα-3-C6-IR	LGQLAAFLHGFYEWFESEAVAA	26.7	21.2	22.0	1.0	1.0	
H2CBα-3-H9-IR	VHSVSRNLNVGFYQWFQDQLSG	23.4	22.5	22.0	1.0	1.0	
H2CBα-3-H8-IR	LGLMAIFDRGFYGMFEQQLSG	23.5	23.4	23.2	1.0	1.0	
H2CBα-3-F2-IR	VARGSSLHDDFYEWFAQLRT	25.5	24.3	25.2	1.0	1.0	
H2CBα-3-D5-IR	LGYIGALNTQFYSWFADLVGS	26.7	24.5	25.6	1.0	1.0	
H2CBα-3-D10-IR	EDSRLRLHEGFYGMFRKQLCD	26.8	24.9	24.9	1.0	1.0	
H2CBα-3-F10-IR	GRDNMKFHSGFYDWFTOQLAG	25.7	25.6	26.1	1.0	1.0	

Figure 1M (Con't)



Clone	Sequence	Ratios over Background				Comparisons	
Design		E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
H2CBa-3-D6-IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	--
H2CBa-3-H3-IR	AGVMGCFHQEFYLMFERALSN	27.9	26.0	25.8	1.0	1.0	1.0
H2CBa-3-F4-IR	AGHVGOVYDGFYGMFREQDLGA	27.0	26.9	26.2	1.0	1.0	1.0
H2CBa-3-E9-IR	FVQNI GFYDGFYGMFVREVEK	31.2	27.2	27.7	1.0	1.0	1.0
H2CBa-3-H10-IR	PVIGIGLHRAFYQWFQSQVDA	31.6	27.7	28.2	1.0	1.0	1.0
H2CBa-3-G2-IR	GSRQEADHQAFYDMFNLVLG	26.9	27.9	28.8	1.0	1.0	1.0
H2CBa-3-B2-IR	AGGRKPFHDDFYGMFRDQLAE	29.1	28.1	28.8	1.0	1.0	1.0
H2CBa-3-E8-IR	DLASHGFHDAFYNMFSVQLNS	29.4	28.1	28.2	1.0	1.0	1.0
H2CBa-3-E5-IR	GSNGGVHQEFYAMFEVALSG	31.5	28.4	29.1	1.0	1.0	1.0
H2CBa-3-E6-IR	RGRASTFHDCFYGMFSQQLRF	33.0	28.7	28.9	1.0	1.0	1.0
H2CBa-3-E7-IR	SPARRVSHHDFYGMFAKQLES	29.6	29.0	28.1	1.0	1.0	1.0
H2CBa-3-C8-IR	SSDVGA FHSAFYDMFKAQLSG	30.4	30.2	30.2	1.0	1.0	1.0
H2CBa-3-A4-IR	PTVHRAFDLDFYGMFAKQVED	31.9	31.2	31.5	1.0	1.0	1.0
H2CBa-3-D1-IR	SSNTVGLDERFYAMFVDQLGA	32.2	31.9	32.6	1.0	1.0	1.0
H2CBa-3-B9-IR	PGAEGFHSAFYDMFAQAVSG	32.9	32.5	31.5	1.0	1.0	1.0
H2CBa-3-F1-IR	MRSEASFHVEFYSMFEEDQLRS	33.2	33.8	33.3	1.0	1.0	1.0
H2CBa-3-A11-IR	VSRYGQDDGFYHMFSDLLKG	26.3	20.2	19.1	1.1	0.9	0.9
H2CBa-3-A3-IR	RPSSGCLHYGFYHMFVRQDEM	28.8	28.0	26.4	1.1	0.9	0.9
	SNIEEHFMQFYRMFSDALGN	20.5	21.5	17.7	1.2	0.8	0.8
	ANDCLGLHAGFYGMFACQLGG	30.4	29.6	21.8	1.4	0.7	0.7

Figure 1M (Con't)





Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	ICfR	IR	ICfR/IR IR/ICfR
H2CB1-3-E8-IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--
H2CB1-4-F8-IR	TGHRGLDGEQFYWWFRDALSG	15.9	1.9	11.8	0.2 6.1
H2CB1-3-C4-IR	VLTSTNLHQRFYSWFAAARE	13.4	0.8	2.6	0.3 3.4
H2CB1-3-D5-IR	CVAQGGFQSSFYCWFAGLDID	21.1	1.3	4.0	0.3 3.1
H2CB1-3-E6-IR	NGQSSRFHTAFYDWFQAQLSG	14.0	3.3	10.2	0.3 3.1
H2CB1-4-G12-IR	SVPRGTVDHAFYQWFRVALG	5.7	0.7	2.1	0.3 3.1
H2CB1-4-F4-IR	GARGSTFHDQFYEMFWQLGD	6.8	1.8	5.4	0.3 3.1
H2CB1-4-F11-IR	PRGMNGFHTSFYSWFVDQLGD	17.9	1.9	5.6	0.3 3.0
H2CB1-3-E5-IR	AVGTLGYHSGFYRWFERQLG	15.0	1.7	4.8	0.3 2.9
H2CB1-4-F2-IR	ELQARGVHRNFYRWFEAQLVSG	17.0	1.8	5.0	0.4 2.8
H2CB1-4-G4-IR	HRVARAFHEQFYDWFKAQVSG	15.9	1.3	3.4	0.4 2.6
H2CB1-3-C8-IR	GAMEPDYHRSFYQWFAAALGE	8.7	1.4	3.5	0.4 2.6
H2CB1-4-F10-IR	CPDRQSVDDRFYNWFADALAS	4.9	1.4	3.2	0.4 2.3
H2CB1-4-H4-IR	GGAQISFHERFYQWFLQEAAG	10.2	1.0	2.4	0.4 2.3
H2CB1-4-G6-IR	HKRGIVQHGAFYAWFDSLSSG	20.8	4.2	9.5	0.4 2.3
H2CB1-4-H1-IR	QASDNRSDDQFYLMFEKLSS	14.5	5.6	8.5	0.7 1.5
H2CB1-4-H1-IR	DRGRMGVDEGFYNWFARQMOE	17.0	10.1	13.2	0.8 1.3

Figure 1M (Con't)



Clone	Sequence	E-Tag	ICFSR	IR	ICFIR/IR	IR/ICFSR
Design	XXXXXXXXXXFXMXFXXXXXX	--	--	--	--	--
Parental	VTFTSAVFHENFYDMFVRQVS	29.8	17.5	16.3	1.1	0.9
H2CB-3-Q2-IGFR	TASQECFDDGFYGMFRAMRCT	22.9	18.6	11.8	1.6	0.6
H2CB-3-C12-IGFR	SLDWRMSEEPFYRMFQRALAG	17.3	19.6	13.0	1.5	0.7
H2CB-3-B11-IGFR	CMSLSDCHRKIFYGMFKSQGGE	24.6	17.1	11.9	1.4	0.7
H2CB-4-E2-IGFR	LALCRSPGSFYGMFQAAVGC	22.4	21.0	16.5	1.3	0.8
H2CB-3-A5-IGFR	PRSATMSDGGFYWMFASQLGL	28.8	26.1	22.6	1.2	0.9
H2CB-4-G12-IGFR	LRRSSVFHDPFYE*ISRLVGG	23.7	23.8	19.4	1.2	0.8
H2CB-3-B2-IGFR	ARLQOQFHGGFYEMFRAQVSP	23.0	19.9	16.4	1.2	0.8
H2CB-3-D1-IGFR	AQLDNLCHPEPFYSWFCVITRE	21.5	19.5	15.7	1.2	0.8
H2CB-3-B6-IGFR	WTCDTAFHQDFYQWFCDKLGV	16.3	4.5	3.7	1.2	0.8
H2CB-4-F7-IGFR	GKEGFGLDRDFYWMFREQLGP	22.0	19.0	18.0	1.1	0.9
H2CB-4-G8-IGFR	GRAPSSFDCDFYCWFRNQVS	20.2	18.6	16.5	1.1	0.9
H2CB-3-D4-IGFR	DVEAETQHRLFYAMFLSQLGS	21.9	18.3	16.9	1.1	0.9
H2CB-3-D5-IGFR	ISVTAVFHDCFYGMFNEQVSK	21.4	17.9	16.4	1.1	0.9
H2CB-4-E6-IGFR	NSEHGRLDVDFYGMFARVIOQ	19.6	15.8	14.8	1.1	0.9
H2CB-3-C2-IGFR	GPLGDCQDGFYGMFCQVST	18.8	12.2	10.8	1.1	0.9
H2CB-3-A6-IGFR	KRSAYNFHDPFYDMFRMQLSG	26.8	29.0	28.1	1.0	1.0
H2CB-4-H12-IGFR	ASEPGGYLDPFYGMFREQLRA	23.9	28.3	28.1	1.0	1.0
H2CB-3-B10-IGFR	NRDGGVHSGFYWMFRLQLSG	27.1	27.5	27.3	1.0	1.0
H2CB-4-F11-IGFR	ASKGSSLHNDFYGMFAOQLAR	25.5	25.5	24.6	1.0	1.0
H2CB-4-G11-IGFR	ANVSMWIOVGFYDMFDAQLRQ	25.3	25.4	25.3	1.0	1.0
H2CB-4-E12-IGFR	RTSPGSLHDPFYDMFQOQLG	27.8	24.9	24.7	1.0	1.0
H2CB-4-G10-IGFR	PGVMSSEFHGGFYSMFREQLNG	25.1	24.6	24.2	1.0	1.0
H2CB-3-B9-IGFR	CLANSEDDHDSFYGMFCQALGG	25.6	23.3	23.7	1.0	1.0
H2CB-3-B7-IGFR	GSGMGGMHGSFYEMFALQLRS	24.0	23.2	23.5	1.0	1.0
H2CB-4-H4-IGFR	RPQGGSIHAGFYQWFRDAVAG	23.5	23.1	23.8	1.0	1.0

Figure 1N

Clone	Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGFSR	IR	IGFSR/IR	IR/IGFSR	
		XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	
H2CB-4-H10-IGFR		GALSSLFDAFYDWFNRQLG	21.9	22.4	23.3	1.0	1.0	1.0
H2CB-4-H5-IGFR		KVDLRGFHDGFGYGMFARQLAG	22.3	22.3	21.6	1.0	1.0	1.0
H2CB-4-G7-IGFR		CSGLQRCHDSFYSWFSVRE	23.1	21.6	20.6	1.0	1.0	1.0
H2CB-4-F4-IGFR		DSLGISFHGFGYDWFRRQLDM	21.3	20.9	21.3	1.0	1.0	1.0
H2CB-3-D8-IGFR		SGVFNGTFYDWFRIQLGE	20.0	20.5	21.6	1.0	1.0	1.0
H2CB-4-E4-IGFR		GYREMRSDLGFYQWFRDQLGL	21.6	20.5	21.2	1.0	1.0	1.0
H2CB-4-E5-IGFR		SVFMQHDHVGFYAMFRSLMEE	22.0	19.9	20.9	1.0	1.0	1.0
H2CB-4-E8-IGFR		FRHITEVDRSFYGMFVEQLRG	21.1	19.7	20.7	1.0	1.1	1.1
H2CB-3-D12-IGFR		WAGGSDVDGSFYDWFQRLLAS	26.6	17.3	16.8	1.0	1.0	1.0
H2CB-4-G9-IGFR		GLQNVSFHSGFYEWFAQVSO	21.6	14.5	15.2	1.0	1.1	1.1
H2CB-3-C8-IGFR		SRVSDPYHVGFYQWFEEVVRG	20.8	13.4	13.9	1.0	1.0	1.0
H2CB-3-A12-IGFR		MGATFFHTGFYDWFPAQLQH	28.6	27.5	29.2	0.9	1.1	1.1
H2CB-3-B12-IGFR		RPASRPFHSGFYQWPAQLSH	27.8	25.2	27.1	0.9	1.1	1.1
H2CB-3-A9-IGFR		GLAPGNFHEDFYRMFQEQTLG	27.7	24.3	25.7	0.9	1.1	1.1
H2CB-3-A3-IGFR		TAAISDFNSLFYGMFEQLSS	26.9	24.1	26.5	0.9	1.1	1.1
H2CB-3-B4-IGFR		LDEDLPQHAGFYGMFAEALGV	25.8	23.8	25.3	0.9	1.1	1.1
H2CB-4-E7-IGFR		ASHKSAFDDNFYRMFSMQLRD	24.6	21.6	24.0	0.9	1.1	1.1
H2CB-4-G6-IGFR		HTGAGDLHGAFYMWFLQQLG	22.4	21.1	23.0	0.9	1.1	1.1
H2CB-4-E9-IGFR		RRGRDGFHGGFYDWFQAQLSD	24.3	20.7	22.0	0.9	1.1	1.1
H2CB-4-H2-IGFR		GNFREAFHADFYSMFERQLQS	21.6	20.2	21.9	0.9	1.1	1.1
H2CB-3-A10-IGFR		RDTLPAFHQHFYQWFEKQVSA	24.3	19.9	21.5	0.9	1.1	1.1
H2CB-3-C4-IGFR		ERETAAFGQAFYQWFRDQIAG	23.1	19.2	22.0	0.9	1.1	1.1
H2CB-3-B5-IGFR		WGEGGGFYDWFYDQLGWPESH	24.2	18.8	20.7	0.9	1.1	1.1
H2CB-4-G4-IGFR		SLVAADLHEGFYGMFRSQLG	21.7	18.7	21.2	0.9	1.1	1.1
H2CB-3-D9-IGFR		TSEVGDFHAEFYSMFEIQLGR	24.4	18.6	20.0	0.9	1.1	1.1
H2CB-3-C3-IGFR		TGADGLLHARFYAMFEEQLRE	20.3	18.4	21.1	0.9	1.1	1.1
H2CB-3-D3-IGFR		RRSDSSLHRSFYDWFVSQLLN	22.5	18.3	21.3	0.9	1.2	1.2
H2CB-4-F2-IGFR		SESKYLLHSGFYGMFEAQLRG	18.0	16.8	18.3	0.9	1.1	1.1

Figure 1N (Con't)



Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFSR	IR	IGFSR/IR/IGFR
	XXXXXXXXXXFXWFXFXXXXXX	--	--	--	--
H2CB-4-H1-IGFR	HGVI RADHTGFGWFSKQUSD	18.3	15.3	16.5	0.9
H2CB-4-F9-IGFR	LINA.VFRRGFYAMFEEQVSK	22.9	14.4	15.3	0.9
H2CB-4-E10-IGFR	LQRYIGFHDPFYDMFSRALSG	26.1	20.1	24.5	0.8
H2CB-4-F8-IGFR	MRTAELFHVGFYDMFDAQLMD	21.5	14.8	19.0	0.8
H2CB-3-A8-IGFR	WAPPDALHGQFYRMFQRQLDQ	20.7	14.7	18.2	0.8
H2CB-4-F1-IGFR	AVHAATFHDPFYRMFEQVVS	22.2	14.6	18.8	0.8
H2CB-3-C6-IGFR	FDAVHGFDCGFGYGMFKRELQR	15.7	7.8	10.2	0.8
H2CB-4-E11-IGFR	QAGMEFHGAFYNNFLOQLSG	26.1	17.6	24.1	0.7
H2CB-3-D6-IGFR	GRSVSRMNAEFYQMFCHQLAA	21.6	13.0	18.8	0.7
H2CB-4-F3-IGFR	AAVNSLFHDEFYLMFQDQLDG	17.3	11.1	16.4	0.7
H2CB-3-A4-IGFR	QLGMDWFHADFYEMFLAQLPS	27.4	11.0	14.8	0.7
H2CB-3-B1-IGFR	RLAGSGIHGFGYGMFVDQLLA	20.0	11.0	15.2	0.7
H2CB-3-C5-IGFR	GREIGGVHDCFYDMFRQOSEQ	19.9	10.5	15.6	0.7
H2CB-4-F6-IGFR	VRSEQRFDSFYQMFNDLMS	18.6	10.1	14.6	0.7
H2CB-3-B8-IGFR	QSPYGFHHDGFGYRMFLQQTGM	20.7	6.9	9.5	0.7
H2CB-3-C7-IGFR	FQCGAAPHVDGYRMFTCOEQF	16.2	1.8	2.5	0.7
H2CB-4-H7-IGFR	GAFGSEFHEQFYRMFEDALSF	21.8	14.1	22.7	0.6
H2CB-4-F5-IGFR	EHTSYQIHRQFYEMFEDRALGR	12.9	4.0	7.2	0.6
H2CB-4-G1-IGFR	SGTAADLSRFGYGMFALQARE	20.4	10.3	19.7	0.5
H2CB-3-D11-IGFR	EGFGVLFHQGYRMFQQLDQ	24.1	8.8	18.6	0.5
H2CB-3-D7-IGFR	QOSAGPHSSFYLMFSELGA	22.1	6.5	13.6	0.5
H2CB-3-C10-IGFR	YLRAGFHRSGFYGMFDQALRD	21.7	5.1	10.4	0.5
H2CB-4-E3-IGFR	MMLWATLHSDFYSWFEQVSG	20.3	4.6	8.9	0.5
H2CB-3-C1-IGFR	CANALGFKDRFYEMFAQLMD	22.3	6.7	15.7	0.4
H2CB-4-G2-IGFR	GSGLYVFHWGFIYDMFEQMG	19.9	3.3	10.7	0.3
H2CB-3-A11-IGFR	LQKMGFDLQFYRMFEAATRA	23.9	2.5	7.7	0.3
H2CB-4-G5-IGFR	QRSAVEFHADFYDMFLRLTLP	19.3	2.5	7.9	0.3
H2CB-4-F12-IGFR	DQRMGSFHGEFYRMFEETLLS	16.7	1.7	5.4	0.3

Figure 1N (Con't)





Clone	Design
	20E2A-3-B11-IR
	20E2B1-3-E3-IR
	1B6-3-F6-IR
	1B6-4-F9-IR
	20E2B4-3-A8-IR
	A6L-4-F6-IR
	20E2B4-4-H9-IR
	20E2B4-3-B1-IR
	20E2B1-4-F9-IR
	20E2B1-3-E9-IR
	20E2B1-3-E10-IR
	20E2B4-3-C12-IR
	20E2B1-3-C12-IR
	20E2B1-3-E7-IR
	20E2B1-3-E11-IR
	20E2B4-3-B11-IR
	NMKH-4-G2-IR
	20E2B4-3-A7-IR
	20E2B4-4-G12-IR
	20E2B4-3-C11-IR
	20E2B4-3-C10-IR

Sequence	$X_n - Fy_{xWF} - X_m$
GRFYGMFQDAIDQLMPWGFDP	
IQWEPFYGMFDDVVAQMFEE	
RYGRWGLAQQFYDWFDR	
RGRLGSLSTQFYNMFAE	
ASAYTPFYQMFADVSEYMQD	
PYRMGTEKWNFYDWFVAQLQ	
SAVHFQFYKMFIDNLLPVLISA	
VPVNKSPFYRMFQDLVLGGSDDW	
QSPRASFYGMFDDVLRACGVV	
TGFYEMFYEQLHSRMLPNPLD	
RGVGGFYGMFSGQLQGMGVA	
SSQDRRFYRMFEQAIVGGRDG	
TRGQLGFYNMFGQALSTSGMG	
CADLNAFYQMFQCGVLDGRSDH	
TLIQDQFYWWFSDDLAEFGD	
IDQLDAFYRMFDGVMGMDP	
RGCGTFYEMFESALRKHGAG	
RGLDQDFYRMFQNLVGEYDR	
MOGHRGFYGMFARVLEQDRGW	
ERLHLRFYEMFDTVIGQDGS	
MHVQSDFYHWFQSLGQGGPD	

Ratios over Background					Comparisons	
E-Tag	ICFSR	IR	ICFR/IR	IR/ICFR		
--	--	--	--	--	--	--
24.6	1.4	23.6	0.1	16.8		
23.0	0.9	15.3	0.1	16.3		
40.9	1.0	13.3	0.1	13.3		
34.1	1.0	12.6	0.1	12.6		
35.4	7.4	34.4	0.2	4.6		
28.9	4.1	18.1	0.2	4.4		
37.8	9.4	26.7	0.4	2.9		
41.8	12.9	36.8	0.4	2.9		
25.9	4.2	10.1	0.4	2.4		
27.0	7.7	17.2	0.5	2.2		
22.2	2.6	5.5	0.5	2.1		
39.0	6.7	12.0	0.6	1.8		
20.2	2.2	3.8	0.6	1.8		
9.2	1.2	1.9	0.6	1.6		
20.7	1.3	2.1	0.6	1.6		
36.0	20.7	32.8	0.6	1.6		
10.8	6.3	8.9	0.7	1.4		
19.0	4.2	5.5	0.8	1.3		
37.0	22.3	29.5	0.8	1.3		
37.3	26.8	34.8	0.8	1.3		
37.7	24.8	30.5	0.8	1.2		

Figure 10



Clone	Sequence $X_n - Fy_{XMF} - X_m$	Ratios over Background				Comparisons	
Design		E-Tag	IGFIR	IR	IGFIR/IR	IR/IGFIR	
20E2Ba-3-D7-IR	TMGTQGFYRMFQNVVKEHILSG	35.4	26.9	31.3	0.9	1.2	
20E2Ba-3-A12-IR	ITHNRGFYSWFLDVVQGAGA	31.7	22.0	23.3	0.9	1.1	
20E2Ba-3-D10-IR	VRRDAGFYQWFADILTLQDFE	32.7	27.3	29.1	0.9	1.1	
20E2Ba-4-G7-IR	MQLQDEFYNNWFRGIMLNDQD	34.2	29.0	30.7	0.9	1.1	
20E2Ba-4-F5-IR	GIRSSGFYQWFDRLVLAGVDCG	33.8	32.1	34.0	0.9	1.1	
20E2Ba-3-C9-IR	ANLNSQFYSMFASVTGEASPS	39.4	33.2	35.5	0.9	1.1	
20E2Ba-4-H10-IR	QSPRASFYGMFDDVLRAGV	38.2	31.6	35.9	0.9	1.1	
20E2Ba-4-E12-IR	MQRNQGFSYSWFDDLVSTVG	36.0	30.8	29.7	1.0	1.0	
20E2Ba-4-E11-IR	ASGFDPFYAMFLEQLRVANGS	35.1	31.2	30.7	1.0	1.0	
20E2Ba-4-E8-IR	SGTPYGFYRMFQSALASATSG	36.1	30.5	30.7	1.0	1.0	
20E2Ba-4-H10-IR	QGEVGGFYEMFDRAMGDVRPM	38.9	30.6	30.7	1.0	1.0	
20E2Ba-4-F6-IR	QNMSCGFYRMFAQVVADSGD	34.9	33.2	32.0	1.0	1.0	
20E2Ba-4-G4-IR	RGTDDTFYGMFDDQLQGMCD	34.1	33.7	32.2	1.0	1.0	
20E2Ba-4-F8-IR	TVDHDTQFYDMFSRVLGSGSA	37.7	32.0	32.7	1.0	1.0	
20E2Ba-4-G5-IR	GRQDREFYWFELQAGMGD	34.9	33.9	33.4	1.0	1.0	
20E2Ba-3-B10-IR	RLLGGFYEMFDQVLKETKEV	38.2	34.9	33.6	1.0	1.0	
20E2Ba-3-C7-IR	GVLSTGFYEMFALQLHGLAAG	37.6	34.2	34.8	1.0	1.0	
20E2Ba-3-C5-IR	PAVGQSFYGMFEAVLRGSKAG	40.4	36.0	35.6	1.0	1.0	
20E2Ba-3-B9-IR	SNGISGFYEMFAAQVQTSDFQ	39.6	35.8	37.1	1.0	1.0	
20E2Ba-4-F11-IR	LLGLSQAYANFYDMFVSQLA	33.1	4.6	4.6	1.0	1.0	
20E2Ba-3-C2-IR	VPNSWMFYNNWFAEQIEGSEGE	44.1	40.0	38.1	1.0	1.0	
20E2Ba-3-B2-IR	ARRADGFYDMFREQVSGSAVQ	43.1	40.1	39.0	1.0	1.0	
20E2Ba-4-G2-IR	GVECTFYEMFDRLLGGVQGD	34.1	33.6	29.8	1.1	0.9	
20E2Ba-4-H6-IR	SHLTDPFYQWFDQLRAGVRC	39.4	36.0	31.9	1.1	0.9	

Figure 10 (Con't)



502877_1

Clone
Design
20E2B α -4-H5-IR
20E2B α -4-G3-IR
20E2B α -4-H4-IR
20E2B α -3-C1-IR
20E2B α -4-E6-IR
H5-3-D5-IR
JBA5-3-D9-IR
20E2B β -4-G6-IR
20E2B β -4-H10-IR
rB6-4-G8-IR

Sequence
 X_n -FyxMF- X_m
RSNDAFYRMFNSNLTQVDGCG
DSDCAQFYIMFEDQLRSAGMD
PGLHRAFYQWFAEAVRSANK \bar{E}
SLGQGGFYDWMFASQVGCADI
CGQTQSFYQWFCCEVMRVESSD
IVVPGDTQGVNFYDWMFVKQLQ
RDVSMGSASTNFYDWMFVQQLG
SQAGSAFYAMFDQVLRIVHSA
SNGISGFYEMFPAQVQTSDFQ
RRDRGGIDVFFYQWFMMD

E-Tag	Ratios over Background		Comparisons	
	IGFIR	IR	IGFIR/IR	IR/IGFIR
--	--	--	--	--
38.7	35.1	32.3	1.1	0.9
35.5	36.1	32.7	1.1	0.9
38.8	37.9	35.0	1.1	0.9
43.7	42.1	39.0	1.1	0.9
38.0	34.3	29.7	1.2	0.9
43.8	21.8	18.2	1.2	0.8
38.3	29.8	25.3	1.2	0.8
22.4	6.2	1.9	3.3	0.3
23.5	32.2	9.7	3.3	0.3
--	--	--	--	--

Figure 10 (Con't)



Clone
Design
R40-3-40H4-IR

Sequence
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RYFPFGGYGNLVDVLRWLRPYVASPRWGHWRPGSLGKQPT

Ratios over Background			Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR
--	--	--	--	--
31.9	1.4	2.1	0.7	1.5

FIGURE 2A

Clone Design
R40-3-B6-IGFR
R40-X-E5-IGFR
R40-X-B5-IGFR
R40-4-9-IGFR
R40-3-G6-IGFR
R40-4-12-IGFR
R40-3-A5-IGFR
R40-X-C6-IGFR

[illegible][illegible]

FIGURE 2B

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGF _{IR}	IR	IGF _{IR} /IR	IR/IGF _{IR}
R20α-4-20C11-IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20α-3-20E2-IR	DRAFYNGLRDLVGAVYGAMD	43.7	30.8	3.0	10.3	0.1
R20α-4-20A12-IR	FYDAIDQLVRGSARAGTRD	46.3	39.9	3.1	12.9	0.1
R20β-4-C6-IR	RLFYCGIGALGANLGYS GCV	48.6	39.9	2.4	16.6	0.1
R20β-4-A6-IR	FYSALWGLCGVTGCG	18.5	28.9	4.3	6.7	0.1
	RGQSDAFYSGLWALIGLSDG	9.3	25.9	1.5	17.3	0.1

FIGURE 2C



Clone Design	Sequence	Ratios over Background				Comparisons	
	XXXXXXXXXXXXXXXXXXXX	E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
R20-4-F11-IGFR	GFYELLGALVGERVNGTNS	39.0	19.2	--	--	--	--
R20-4-C7-IGFR	ERTDPFYKALLSLGGDGS	33.4	17.5	--	--	--	--
R20-3-F2-IGFR	DVQNGSSGFYDGI FGLAWG	31.8	14.3	--	--	--	--
R20-4-A11-IGFR	PFYVWIRDLLGPELPHTRGD	37.8	13.5	--	--	--	--
R20-4-B12-IGFR	VLVVGGLDPFYEGGLHRLIS	37.2	10.0	--	--	--	--
R20-4-B10-IGFR	GFYRLNELVREGGALKVGA	37.0	9.5	--	--	--	--
R20-4-E9-IGFR	GQRGFYELLSELLGHEGVF	34.2	9.4	--	--	--	--
R20-3-H4-IGFR	DWVGPFYRCIELLSGFQIE	30.3	7.8	--	--	--	--
R20-3-G2-IGFR	GGSLFYEGLLRLVLGDSVVG	20.8	6.9	--	--	--	--
R20-4-B8-IGFR	LNHFYAMLSDLSCVRNIFPG	32.8	6.5	--	--	--	--
R20-4-E7-IGFR	LSGFYEGLFRLARRDGSWG	35.4	6.4	--	--	--	--
R20-4-G9-IGFR	FYDVL SALVGE LGEQGDAS	25.0	6.4	--	--	--	--
R20-4-D9-IGFR	GAGSFGREGGFYEALMQLAG	23.4	6.3	--	--	--	--
R20-4-D11-IGFR	DDEFYSQILKLVDSRGGRSGTON	31.3	4.0	--	--	--	--
R20-4-G10-IGFR	PFYMLLSRLVGVEQEGL	13.6	3.3	--	--	--	--
R20-4-C8-IGFR	FYDAIDQLVRSARAGCTRD	16.8	3.2	--	--	--	--

FIGURE 2D





Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGfsR	IR	IGFR/IR	IR/IGFR	
20C-3-G3-IGFR	XXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	--
20C-4-C7-IGFR	TFYSCLASJLTGTPQPNRGPMWRCR	33.1	32.3	1.2	27.0	<0.1	
20C-3-F6-IGFR	FFYDCLAALLQGVARYHDLCAVEIT	35.3	28.0	1.3	21.8	<0.1	
20C-3-A1-IGFR	DRDFCRFYERLTALVGGQVDGWPQ	33.5	26.1	1.9	14.1	0.1	
20C-3-A4-IGFR	SSYGCDGFYLMFLSLGLVASQLEEC	26.5	20.8	1.5	13.7	0.1	
20C-3-E4-IGFR	QFYGCLLDLSLGVPSFGWRRRCITA	17.7	8.8	1.2	7.6	0.1	
20C-4-D11-IGFR	FFYRCLSRLLGGQLGSRLLGSCI GD	37.7	7.7	1.3	6.0	0.2	
20C-4-F7-IGFR	DLFYCMNMQLATAGVCGSLGSPVCG	33.3	17.2	6.1	2.8	0.4	
20C-3-B2-IGFR	GSACDGFYACLHALVQGPGEW	31.2	28.9	17.0	1.7	0.6	
		37.7	35.2	30.9	1.1	0.9	

FIGURE 2E



Clone
Parental/Design
B6L-4-C8-IR
B6L-4-B7-IR
B6L-3-H1-IR
B6L-4-E12-IR
B6L-4-D8-IR
B6L-4-F7-IR
B6L-4-B11-IR
B6L-4-B12-IR
B6L-4-B8-IR
B6L-4-E8-IR
B6L-3-G6-IR
B6L-3-G5-IR
B6L-4-E10-IR
B6L-4-F10-IR
B6L-3-F3-IR
B6L-4-A7-IR
B6L-4-G8-IR
B6L-4-F8-IR
B6L-4-G7-IR
B6L-3-F4-IR
B6L-3-H4-IR
B6L-3-A6-IR
B6L-4-D7-IR
B6L-3-E2-IR

Sequence
AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA
ANLRLR?VGNRL*SVMPGEQWNTVDPFYOKLYELVRESGA
AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGD
AETPAHVC*TVGGLFGRVNTWNTVDPFYAKLSELLRESGA
GQNSGSAMDGISLMSVMPGDVWNPVDPFYHKLSELLRESGA
AETPAQVGWNLQGEHMTVDPFYHKLSELLRESGA
AETPAQVGWNLMSVMPGEH*NTVDPFYHKLSELLRESGD
AETPAQVGQNLMSVMPGEHMTVDPFYOKLSELLRESGA
AETPAQVGQNLMSVMPGELMTVDPFYHKLSELLRESGA
T*QGETPAQVSLMPGEHMTVDPFYHKLSELLRESGA
QGETPAQIGWNPPLMSVMPGEHMTLDPFYHKLSELLRESGA
VDTPAQVGWNRRLMSVMPGEHMTDPPFYH*LSELLRESGA
AETSAQVGWQRLMSVMPGDHMTDPPFYHKLSELLRESGA
*NSPRVGNGLMSVMPGEHMTDPPFYHKLSELLRESGV
AETPAQIGWNRRLMSVMPGEHMTVDPFYHKLSELLRESSP
ADTPAQVSGNRRLMSVMPGDPWNTVDPFYHKLSELLRESGA
AGTPAQVG*NRLMSVMPGEHMTVDPFYHKLSELLRESGA
D*QAWSVMPGQHMTIDPFYHKLSELLRESGA
AETLARVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA
AATRPQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGS
LITPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA
ADNPAQVGWNRRLMSVMPVEH*NTVDPFYHKLSELLRESGA
AETPAQVGWNRRLMSVMPGCHMTLDPFYHKLSELLRESGA
AETSVQVGWIRLMSVMPGEHMTVDPFYHKLSELLRESGA
G*NSAHVGWNRRLMSVMPGEHMTVDPFYHKLSELLRVSOG

Ratios over Background		Comparisons	
E-Tag	ICFSR	IR	ICFR/IR
--	--	--	--
40.5	6.1	40.8	0.2
19.6	4.0	23.5	0.2
20.6	2.8	2.7	0.9
15.5	4.1	3.0	1.1
36.0	9.4	8.5	1.1
37.8	24.6	20.6	1.2
5.5	2.0	1.6	1.3
6.8	2.0	1.6	1.3
36.4	18.7	14.2	1.3
35.6	11.4	8.6	1.3
7.6	2.5	1.8	1.4
11.5	2.0	1.4	1.4
14.8	3.2	2.2	1.5
26.2	11.5	7.2	1.6
36.0	17.1	10.1	1.7
11.6	3.4	1.9	1.8
30.4	11.2	5.9	2.0
35.6	12.8	7.2	2.0
33.5	12.9	6.4	2.3
16.9	6.3	2.7	2.4
20.6	4.9	2.0	2.5
22.4	6.3	3.2	3.2
14.3	4.8	1.4	3.4
29.2	16.7	3.8	6.3

FIGURE 2F



Clone	Sequence	Ratios over Background		Comparisons	
		F-Tag	IGFSR	IR	IGFSR/IR/IGFSR
D #1gn	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	--	--	--	--
B6L-4-G6-IGFR	AETPAQVGCDRLMSVMPGEHMTVDPFYHKLSELLRESGA	7.3	22.1	--	--
B6L-4-G10-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	5.5	21.8	--	--
B6L-4-G3-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	5.8	18.1	--	--
B6L-3-F10-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	6.7	17.4	--	--
B6L-4-D2-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	6.5	15.9	--	--
B6L-3-H10-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	5.9	15.2	--	--
B6L-4-B12-IGFR	DETSAPQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	6.3	14.8	--	--
B6L-3-A9-IGFR	GETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	5.2	14.8	--	--
B6L-4-C4-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	5.4	11.9	--	--
B6L-4-E3-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	4.4	11.1	--	--
B6L-4-A12-IGFR	PETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	3.0	10.4	--	--
B6L-4-D5-IGFR	AQTPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	4.7	10.3	--	--
B6L-3-A10-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	10.9	9.7	--	--
B6L-3-B9-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	2.9	9.1	--	--
B6L-3-H9-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	4.5	8.8	--	--
B6L-4-A5-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	2.4	8.0	--	--
B6L-3-H11-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	4.2	7.5	--	--
B6L-3-G10-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	2.5	7.4	--	--
B6L-4-D4-IGFR	DETPAHVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	2.4	6.8	--	--
B6L-4-F11-IGFR	AGTPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	2.1	6.4	--	--
B6L-4-F12-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	2.7	5.9	--	--
B6L-4-E12-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	1.9	3.9	--	--
B6L-4-E10-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	1.8	3.6	--	--
B6L-3-G9-IGFR	AETPAQVGWNRRLMSVMPGEHMTVDPFYHKLSELLRESGA	1.2	2.5	--	--

FIGURE 2C



Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFSR	IR	IGFSR IR/IGFSR
B6Hq-3-F5-IR	00UUUUUUUUJJJDDPFYHKLSELXXOO	42.7	9.6	17.9	0.5 1.9
B6Hq-2-D10-IR	GGAVAAAVGSRADPFYHKLSELVQGS	20.8	1.7	1.1	1.5 0.6
B6Hq-3-F1-IR	SGGQQRKAIAITSDDPFYHKLSELLG	22.5	2.4	1.3	1.8 0.5
B6Hq-3-E6-IR	CSMAVAEAGDDDDPFYHKLSELQGS	18.2	2.3	1.2	1.9 0.5
B6Hq-1-B8-IR	CGAKMTGTNPDPFYHKLSELLORG	44.6	5.2	2.1	2.5 0.4
B6Hq-2-D5-IR	CCVEAEBAVGRGDPFYHKLSELTGCC	39.6	2.3	0.9	2.6 0.4
B6Hq-1-B3-IR	SRVVTMVIKRGSPDPFYHKLSELVQGR	33.1	3.2	1.1	2.9 0.3
B6Hq-3-E5-IR	GCITAENGAGDPFYHKLSELGGS	28.8	2.9	1.0	2.9 0.3
B6Hq-4-H9-IR	RCGDEEGWQENRRDDPFYHKLSELFGC	17.4	6.4	2.1	3.0 0.3
B6Hq-2-D8-IR	GCEVIAAEGRRDDPFYHKLSELQGG	19.3	3.0	1.0	3.0 0.3
B6Hq-3-E4-IR	SSETAKMVTGTRDDPFYHKLSELVQGS	43.1	8.7	2.8	3.1 0.3
B6Hq-3-F7-IR	WLCDGWMKQRRPPGDPFYHKLSELIDCG	41.5	3.1	1.0	3.1 0.3
B6Hq-1-A3-IR	SRVAATKEKRPSDDPFYHKLSELLQGS	37.4	2.6	0.8	3.3 0.3
B6Hq-4-H10-IR	SGRAKVEAEMPDSGDPFYHKLSELLASG	50.5	29.5	8.6	3.4 0.3
B6Hq-3-F6-IR	GGAAKTIVGSPDDPFYHKLSELLQGS	48.9	19.7	5.7	3.5 0.3
B6Hq-3-F3-IR	CGVGEQMEVTDGDDPFYHKLSELLWSC	18.1	15.6	4.3	3.6 0.3
B6Hq-4-G8-IR	SGEQTATIEGPNDDPFYHKLSELLWGS	32.3	6.1	1.7	3.6 0.3
B6Hq-2-D1-IR	GGTKAVAKVGTTRDDPFYHKLSELLQGS	11.7	5.4	1.3	4.2 0.2
B6Hq-3-E7-IR	GCEVIVEEGDSADPFYHKLSELQGS	47.0	5.6	1.3	4.3 0.2
B6Hq-2-D6-IR	GCAVVEEAERSRGDPFYHKLSELVQGG	33.5	4.4	1.0	4.4 0.2
B6Hq-3-F10-IR	GRTMAVMAAGPDDPFYHKLSELLQGS	47.2	8.8	1.9	4.6 0.2
B6Hq-2-C10-IR	GCVVEWQKWHGASDPFYHKLSELLGGS	47.6	5.3	1.1	4.8 0.2
B6Hq-2-C7-IR	RGKTAAVIVGRPADPFYHKLSELLQGG	46.9	5.8	1.1	5.3 0.2
	SGAKIVVTGDSGDPFYHKLSELLQGS	45.1	6.7	1.0	6.7 0.1
	RGIVAMVEATEVGS DHPFYHKLSELVQGS				

FIGURE 2H

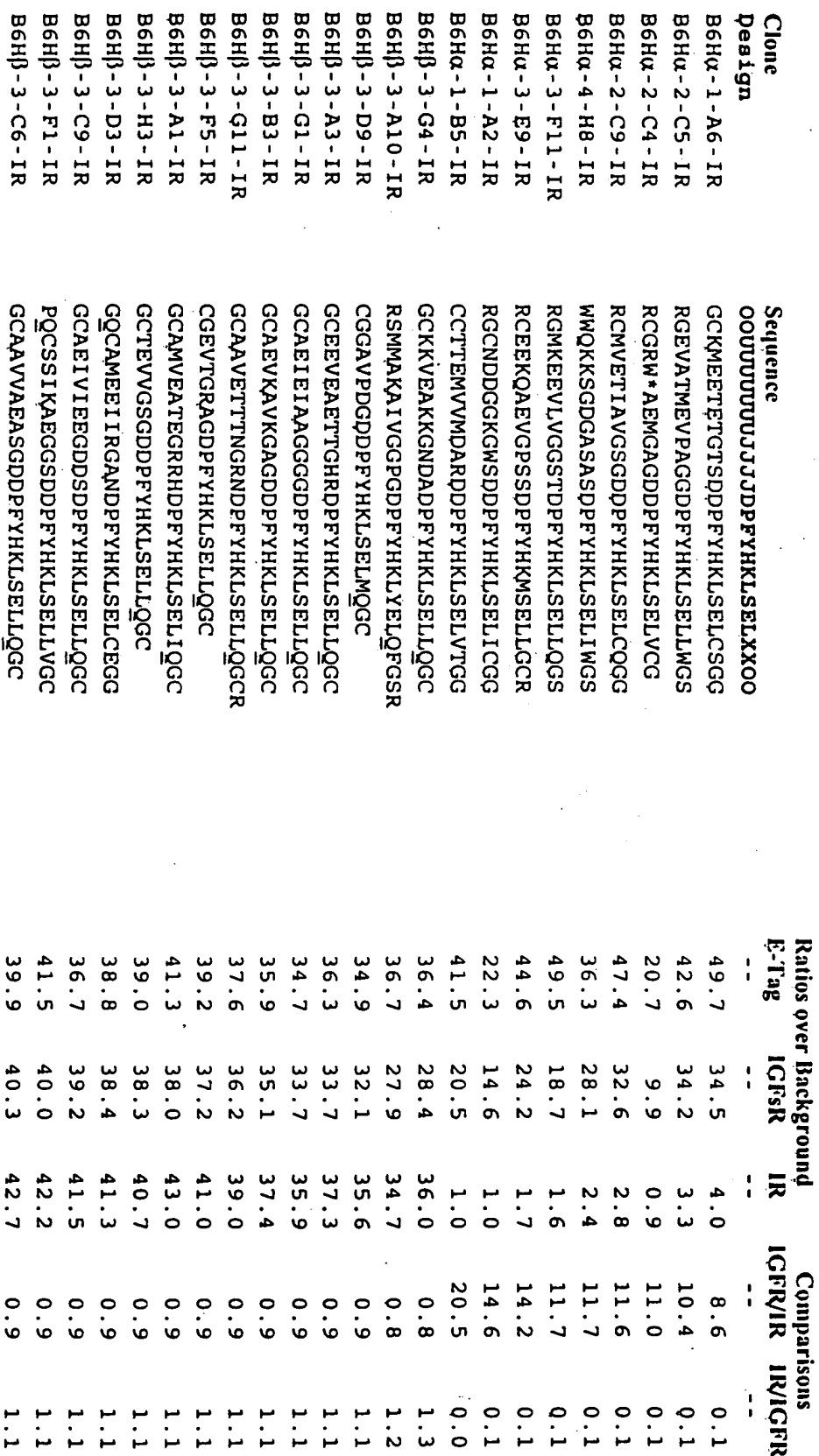


FIGURE 2H (Con't)



Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFSR	IGFR/IR	IR/IGFR
B6HJ-3-D7-IR	OOUUUUUUJJJDPFYHKLSELXXOO	39.5	27.1	26.3	1.0
B6HJ-3-B2-IR	RGVEMKAIIVGTPNDPFYHKLSELSSGS	34.3	34.4	35.4	1.0
B6HJ-3-G5-IR	CSAVKMAEAGDPSDPFYHKLSELQCGS	35.3	35.0	35.6	1.0
B6HJ-3-H1-IR	RGCGDPFYHKLSELMQSS	36.8	35.4	36.5	1.0
B6HJ-3-A5-IR	WLCKRQTHDPDPFYHKLSELACGR	34.9	35.5	35.9	1.0
B6HJ-3-H11-IR	SSKVVKATVGTPHDPFYHKLSELQGS	37.7	36.4	37.6	1.0
B6HJ-3-C2-IR	GCAAIATGNDNDPFYHKLSELQGR	37.4	36.5	37.2	1.0
B6HJ-3-C8-IR	GCAAVKETHPDPDPFYHKLSELHGC	37.0	37.7	39.5	1.0
B6HJ-3-A11-IR	SCAEKEVAGTARDPFYHKLSELMQSS	40.4	38.2	39.1	1.0
B6HJ-3-B7-IR	CSVAVGDSGDPFYHKLSELQGR	35.4	38.3	39.5	1.0
B6HJ-3-B4-IR	WQRNKQOIIGTPDDPFYHKLSELLEGS	37.8	39.0	39.4	1.0
B6HJ-3-A12-IR	RSAAKAVIGSPNDPFYHKLSELQGG	33.5	39.4	41.3	1.0
B6HJ-3-B8-IR	WLCDRDGRDEQPMWDPFYHKLSELVSCGR	39.0	39.8	41.1	1.0
B6HJ-3-A4-IR	GSAVAAKKTGSDDPFYHKLSELLQGS	40.1	40.4	41.1	1.0
B6HJ-3-E12-IR	GCAVTMTMRSRDPFYHKLSELQGR	35.8	40.7	40.7	1.0
B6HJ-3-B5-IR	GCKVDE*AKSSDPFYHKLSELKGR	40.8	40.7	39.5	1.0
B6HJ-3-C5-IR	GCKAVEVKDHGDDPFYHKLSELQGC	40.7	40.9	42.6	1.0
B6HJ-3-A2-IR	CSTVTVSGSDDPFYHKLSELQGC	41.1	41.4	41.9	1.0
B6HJ-3-A8-IR	RSVTAKVEVGSRRDPFYHKLSELQGS	40.0	41.9	41.6	1.0
B6HJ-3-C12-IR	GSRROKIEVGTPNDPFYHKLSELQGG	39.8	42.0	41.3	1.0
B6HJ-3-B11-IR	LCDEKQRTGCTNDPFYHKLSELTGGR	40.7	42.6	43.3	1.0
B6HJ-3-C3-IR	SCMVEGPNDDPFYHKLSELLQGR	43.0	42.7	44.0	1.0
B6HJ-3-B5-IR	GGAIVVAMGNDDPFYHKLSELMQGS	42.7	43.9	45.4	1.0
B6HJ-3-C4-IR	GGVIKAMKAGRPDDPFYHKLSELLDCG	41.1	42.3	36.6	0.9
B6HJ-3-G7-IR	GCEKVVAVAGNAGDPFYHKLSELLQGC	4.1	2.4	2.1	0.9
B6HJ-3-C11-IR	GSMVTVTMAGADDPFYHKLSELLQGR	29.2	30.6	28.2	0.9

FIGURE 211 (Con't)

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR
	00UUUUUUUUJJJJPPFYHKLSELXX00	--	--	--	--	--
B6H3-3-H12-IR	RGEAKKAKIGSAGDPFYHKLSELMQGR	33.6	32.0	29.5	1.1	0.9
B6H3-3-G10-IR	GCEEVVVMANSSADPFYHKLSELCQGR	30.1	34.3	30.5	1.1	0.9
B6H3-3-F10-IR	GCAAVVVTGGDNDFYHKLSELLQGR	37.1	35.3	32.4	1.1	0.9
B6H3-3-D5-IR	SRTGERQVNGSHADPFYHKLSELLSS	39.9	38.9	35.5	1.1	0.9
B6H3-3-B12-IR	GCKEVVETAHADDPFYHKLSELLQGR	39.5	40.0	37.1	1.1	0.9
B6H3-3-D2-IR	RRITIKVKAGDDDDPFYHKLSELLMG	40.4	41.5	39.1	1.1	0.9
B6H3-3-D1-IR	WCDQKETVNSDDPFYHKLSELVGCS	41.1	44.6	36.6	1.2	0.8
B6H3-3-G6-IR	RCEEITIGDGRAGDPFYHKLSELLQGC	34.3	36.4	24.1	1.5	0.7
B6H3-3-A7-IR	CSVMTTEKNDRRDDPFYHKLSELLQGC	38.1	30.9	18.4	1.7	0.6
B6H3-3-B10-IR	GGEARRRQGVGTANDPFYHKLSELAFGGR	32.3	36.5	22.8	1.6	0.6
B6H3-3-B9-IR	GCAVTAITINGTSDDPFYHKLSELCQGS	38.6	38.5	20.8	1.9	0.5
B6H3-3-D6-IR	GSKVKAMAVGTSDDPFYHKLSELVQGR	35.9	36.0	15.6	2.3	0.4
B6H3-3-C7-IR	RCKGIKAHSDNDPFYHKLSELCQGG	38.3	38.0	6.6	5.8	0.2

FIGURE 2H (Con't)





Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tig	IGFSR	IR	IGFR/IR	IR/IGFR
B6H-3-F1-IGFR	OOUUUUUUJJJJDPFYHKLSELXXOO	--	----	--	--	--
B6H-3-D4-IGFR	RRVAAVA?KDATGDPFYHKLSELLRSRG	20.0	30.8	--	--	--
B6H-3-G3-IGFR	RSTMKEKIEGDNDPFYHKLSELLKSG	19.0	27.6	--	--	--
B6H-3-F2-IGFR	GGAVIVTARRGSDPFYHKLSELVGRG	14.2	25.2	--	--	--
B6H-3-D1-IGFR	SREAVEVTMRGSDPFYHKLSELVGSG	12.5	24.8	--	--	--
B6H-3-A3-IGFR	RSTMVKAVPPPRDPFYHKLSELL*GG	20.0	24.2	--	--	--
B6H-3-A4-IGFR	GRTEEVVVGTRDPFYHKLSELLASG	14.2	22.8	--	--	--
B6H-3-B4-IGFR	RRMAGWQ*TSSSDPFYHKLSELVSGS	13.0	22.8	--	--	--
B6H-4-D11-IGFR	SRKEVTEMVGGPSDPFYHKLSELMGSG	10.2	22.8	--	--	--
B6H-3-G2-IGFR	RGTAKQKSSDP*DPFYHKLSELIYGS	14.0	22.5	--	--	--
B6H-3-B2-IGFR	GGVAVVAAGRDDPFYHKLSELVSGR	15.2	22.5	--	--	--
B6H-3-E2-IGFR	SR.MAMVEVGNPGDPFYHKLSELLGSG	14.5	21.9	--	--	--
B6H-3-B1-IGFR	RRVTAVIEVDGADDPFYHKL?ELLSGG	11.6	21.8	--	--	--
B6H-4-G3-IGFR	RSVIAN?G?NADPFYHKLSELLISSG	15.9	21.7	--	--	--
B6H-4-F9-IGFR	RGVVIETTKDPCADPFYHKLSELLFGR	19.1	21.4	--	--	--
B6H-3-E3-IGFR	RRTVMETVGGRDDPFYHKLSELLHRG	11.3	20.9	--	--	--
B6H-3-E1-IGFR	GRVVVAAAVRPDDDPFYHKLSELVAGR	14.2	20.8	--	--	--
B6H-4-F3-IGFR	RGVATVVANHSDPFYHKLSELVLRG	20.0	20.6	--	--	--
B6H-3-D2-IGFR	RRKMATEIMRSDADPFYHKLSELLGSG	12.5	20.3	--	--	--
B6H-4-A9-IGFR	GKTAVENTSPASDPFYHKLSELLLRG	12.1	19.3	--	--	--
B6H-4-E6-IGFR	RREKKVKVTTTNDNPFYHKLSELLVFGG	14.1	19.2	--	--	--
B6H-4-C3-IGFR	SSAIIIMVAADRADDPFYHKLSELLMGS	12.5	19.2	--	--	--
B6H-3-C4-IGFR	RREVAIIVAAGAGDDPFYHKLSELLSRG	23.6	18.9	--	--	--
B6H-3-B3-IGFR	RRVMEAAENHADDPFYHKLSELLWRD	16.2	18.5	--	--	--
B6H-4-H3-IGFR	GRKMEIVAIRGAHDPFYHKLSELL*GR	16.8	17.2	--	--	--
B6H-3-H3-IGFR	CCIAMVEMAAGGDDPFYHKLSELLSGR	14.6	17.1	--	--	--
B6H-3-H3-IGFR	RGAQSPDPFYHKLSELL*GG	9.0	16.8	--	--	--
B6H-3-H3-IGFR	RKTAMVIVIGDASDPFYHKLSELL*GG	10.1	16.6	--	--	--
B6H-3-H3-IGFR	GSVITKAMKADGDDPFYHKLSELL*GG	14.2	16.4	--	--	--

FIGURE 21



Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGfSR	IR	IGfR/IR	IR/IGfR	
B6H-4-D8-IGFR	OOYUUUUUUJJJDDPFYHKLSELXXOO	--	--	--	--	--	--
B6H-4-D6-IGFR	GGVKA AAAERDDSDPFYHKLSEL LFGS	15.1	16.4	--	--	--	--
B6H-4-E10-IGFR	CCEMVKTI EHGCNDPFYHKLSELV FGR	12.6	15.6	--	--	--	--
B6H-4-F5-IGFR	GGAKVAVVDHGD DPFYHKLSEL RGS	10.2	15.1	--	--	--	--
B6H-4-B2-IGFR	RGKTMA MAAGNRDPFYHKLSEL I FGN	12.3	14.8	--	--	--	--
B6H-3-F3-IGFR	GGMATKI VTA PGHDPFYHKLSEL LFGG	6.6	11.8	--	--	--	--
B6H-3-A2-IGFR	SGEGEMAMPD DPFYHKLSELV GCG	8.2	11.6	--	--	--	--
B6H-3-H2-IGFR	GGMAEVVVVG PPRDPFYHKLSELV GCG	10.9	9.9	--	--	--	--
B6H-4-A1-IGFR	GGEVKVMVADG STDPFYHKLSELV GRT	5.9	9.6	--	--	--	--
B6H-3-H1-IGFR	SCVMETVAGNRD PFYHKLSELV GCG	4.4	9.5	--	--	--	--
B6H-4-C2-IGFR	RRW*KVPGAD PFYHKLSEL LGRSA	7.2	8.7	--	--	--	--
B6H-4-B7-IGFR	GGVEATEVEHAD GDPFYHKLSELV GRS	6.7	8.6	--	--	--	--
B6H-4-B4-IGFR	RGVEVAVITHG PDPFYHKLSEL LRG	12.3	8.4	--	--	--	--
B6H-4-A7-IGFR	SGTVTVIAMS GTD DPFYHKLSEL LRS	6.4	8.2	--	--	--	--
B6H-4-B3-IGFR	GRTAVVKEAS PAHDPFYHKLSEL LRG	9.7	8.1	--	--	--	--
B6H-4-B4-IGFR	RGAIGNAAVGN RSDPFYHKLSEL LRS	4.4	7.8	--	--	--	--
B6H-4-E1-IGFR	GGMIKTAMEH DTRDPFYHKLSEL LRG	5.2	7.4	--	--	--	--
B6H-3-C1-IGFR	GCAEVEEVAGAC GHDPFYHKLSELV ?SG	3.6	7.1	--	--	--	--
B6H-4-A3-IGFR	SSVVVEVVDAR DDPFYHKLSEL LRS	5.7	4.6	--	--	--	--
B6H-4-H10-IGFR	GRKKA VATMTD GDDPFYHKLSEL LRG	4.4	4.2	--	--	--	--
B6H-3-G1-IGFR	RGETEMAVAD TDDDPFYHKLSEL LRG	4.4	3.2	--	--	--	--
	GQRDPFYHKLSEL MGRGA	2.4	2.9	--	--	--	--

FIGURE 21 (Con't)



Clone	Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
		EHWNTVDPFYHKISELLRESG	--	--	--	--	--	--
B6C-3-C7-IR		EHWNTVDPFYFTLFE*LRRESG	31.7	2.1	20.0	0.1	9.4	
B6C-4-F2-IR		EHWNTVDPFYQGLWELWELRESG	8.2	1.8	4.3	0.4	2.4	
B6C-3-A2-IR		EHWNTVDPFYHQLSWELWELRESG	34.9	18.1	36.0	0.5	2.0	
B6C-4-H11-IR		EHWNTVDPFYQGLYEWELWELRESG	37.1	28.2	38.6	0.7	1.4	
B6C-4-H4-IR		EHWNTVDPFYRQLSEWELWELRESG	39.5	28.3	39.4	0.7	1.4	
B6C-3-A11-IR		EHWNTVDPFYHYFQELWELRESG	25.4	25.9	34.2	0.8	1.3	
B6C-3-D9-IR		EHWNTVDPFYHQMYEWELWELRESG	35.7	30.3	37.2	0.8	1.2	
B6C-4-G4-IR		EHWNTVDPFYRQLYEWELWELRESG	35.3	31.0	38.4	0.8	1.2	
B6C-3-C6-IR		EHWNTVDLFYQGLQELWELRESG	33.3	33.9	35.9	0.9	1.1	
B6C-3-D8-IR		EHWNTVDPFYH*ISELLRESG	34.5	34.7	37.1	0.9	1.1	
B6C-4-G7-IR		EHWNTVDPFYQFFAELWELRESG	35.9	36.9	38.9	0.9	1.1	
B6C-3-C8-IR		EH*NTVDPFYEGLELLRESG	35.6	37.2	39.6	0.9	1.1	
B6C-3-D6-IR		EH*NTVDPFYQGLFELLRESG	37.6	37.6	40.2	0.9	1.1	
B6C-3-C10-IR		EHWNTVDPFYQYFSELLRESG	35.3	36.4	40.6	0.9	1.1	
B6C-3-B3-IR		EHWNTVDPFYQGLQTLRESG	38.3	38.7	40.8	0.9	1.1	
B6C-3-B1-IR		EHWNTVDPFYQALFELLRESG	37.8	38.9	41.2	0.9	1.1	
B6C-4-F6-IR		EHWNTVDPFYD*MRNLLRESG	35.8	36.8	38.7	1.0	1.1	
B6C-3-B11-IR		EHWNTVDPFYNNLQELWELRESG	36.3	37.0	38.8	1.0	1.1	
B6C-3-B8-IR		EHWNTVDPFYDGLRQLRESG	37.2	39.2	41.2	1.0	1.1	
B6C-3-C12-IR		EHWNTVDPFYQGLQELWELRESG	28.3	28.7	28.9	1.0	1.0	
B6C-3-C2-IR		EHWNTVDPFYQGLFELLRESG	34.1	34.7	33.8	1.0	1.0	
B6C-3-D5-IR		EHWNTVDPFYMLQQLRESG	33.9	35.3	34.1	1.0	1.0	
B6C-4-F7-IR		EH*NTVDPFYHKLVELRESG	34.9	34.7	34.2	1.0	1.0	
B6C-4-H2-IR		EHWNTVDPFYH*MSNLLRESG	35.4	35.8	35.8	1.0	1.0	
B6C-3-B12-IR		EHWNTVDPFY*MSSELLRESG	33.6	35.2	36.0	1.0	1.0	
B6C-3-A12-IR		EHWNTVDPFYQLLFELLRESG	33.1	37.0	36.2	1.0	1.0	
B6C-4-E9-IR		EHWNTVDPFYQRMFELLRESG	36.1	36.0	36.2	1.0	1.0	
B6C-4-E8-IR		EHWNTVDPFYQGLWELWELRESG	34.2	35.0	36.6	1.0	1.0	

FIGURE 2J



Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF _{SR}	IR	IGF _{IR} /IR
B6C-3-C11-IR	EHWNTVDPFYHKLSELLRESG	33.4	35.0	36.7	1.0
B6C-3-C4-IR	EHWNTVDPFYHLLQELLRESG	34.5	35.2	36.8	1.0
B6C-3-B6-IR	EHWNTVDPFYHMLQELLRESG	34.2	36.1	36.9	1.0
B6C-4-E5-IR	EHWNTVDPFYH*MSDLLRESG	35.5	35.8	36.9	1.0
B6C-4-H12-IR	EHWNTVDPFYHYLQDLLRESG	37.0	36.2	37.1	1.0
B6C-4-F9-IR	EHWNTVDSFYHGLQELLRESG	36.1	36.2	37.3	1.0
B6C-3-A6-IR	EHWNTVDPFYQGLSELLRESG	35.8	38.0	37.4	1.0
B6C-3-D1-IR	EHWNTVDPFYQALQQLRESG	36.2	37.8	37.5	1.0
B6C-3-D4-IR	EHWNTVDPFYLMQDLLRESG	35.9	36.4	37.5	1.0
B6C-3-C1-IR	EHWNTVDPFYHKLQDLLRESG	36.8	36.6	37.9	1.0
B6C-4-G5-IR	EHWNTVDPFYQKLQELLRESG	36.5	37.9	38.0	1.0
B6C-3-A8-IR	EHWNTIDPFYHQISELLRESG	34.4	37.0	38.1	1.0
B6C-4-H1-IR	EHWNTVDPFYH*MTPELLRESG	36.8	36.5	38.3	1.0
B6C-3-D10-IR	EHWNTVDPFYHYMSQLLRESG	37.0	37.0	38.5	1.0
B6C-3-D12-IR	EHWNTVDPFYQGLFELLRESG	36.2	37.0	38.7	1.0
B6C-3-B9-IR	EHWNTVDPFYAKLQELLRESG	36.3	37.3	38.8	1.0
B6C-4-H7-IR	EHWNTVDPFYH*MRLLRESG	37.5	38.0	39.1	1.0
B6C-3-D11-IR	EHWNTVDPFYHGL*ELLRESG	36.1	37.5	39.2	1.0
B6C-4-F10-IR	EHWNTVDPFYHGLQELLRESG	37.9	38.6	39.3	1.0
B6C-4-G8-IR	EHWNTVDPFYD*IADLLRESG	35.9	38.0	39.7	1.0
B6C-3-A9-IR	EH*NTVDPFYHGLYELLRESG	36.5	38.8	39.9	1.0
B6C-3-A7-IR	EHWNTVDAFYHGLQELLRESG	38.1	39.4	40.2	1.0
B6C-4-F12-IR	EHWNTVDPFYQGLIELLRESG	38.0	38.4	40.2	1.0
B6C-4-G9-IR	EHWNTVDPFYQGLDLLRESG	37.5	39.4	40.5	1.0
B6C-4-H8-IR	EHWNTVDPFYQGLDLLRESG	38.5	40.0	40.8	1.0
B6C-3-B10-IR	EHWNTVDPFYQKLQDLLRESG	39.3	40.3	40.9	1.0
B6C-3-A10-IR	EHWNTVDPFYHGLQELLRESG	38.4	40.9	41.6	1.0
B6C-3-A3-IR	EHWNTVDPFYH*MSELLRESG	39.2	40.0	41.7	1.0
B6C-3-A5-IR	EHWNTVDPFYAGLQALLRESG	38.2	40.4	41.9	1.0
B6C-3-C3-IR	EHWNTVDPFYHMLQKLLRESG	34.5	34.6	32.0	0.9

FIGURE 2J (Con't)



Clone
Design
B6C-4-F4-IR
B6C-3-D2-IR
B6C-3-A1-IR
B6C-3-B5-IR
B6C-3-A4-IR

Sequence
EHMNTVDPEFYHKLSELLRESG
EHMNTVDPEFYHKLSELLRESG
EHMNTVDPEFYH*LAELLRESG
EHMNTVDPEFYH*LNEILLRESG
EHMNTVDPEFYHKLQELLRESG
EHMNTVDPEFYRLQELLRESG

Ratios over Background				Comparisons	
E-Tig	IGFSR	IR	IGFR/IR	IR/IGFR	
--	--	--	--	--	--
36.3	36.9	34.3	1.1	0.9	
8.5	10.3	9.0	1.2	0.9	
26.5	30.7	16.8	1.8	0.5	
33.4	33.0	15.0	2.2	0.5	
33.6	31.8	13.5	2.4	0.4	

FIGURE 2J (Con't)

Clone B6

AETPAQVGWNR~~L~~MSVWPGEHWNTVDPFYHKLSELLRESGA

Peptide 5.1 (18 aa)

NTVDPEFYHKLSELLREKK (biotin)

Clone F6

MLLGVLRFQILLWPFPPKDCVQMKDIFYSLASL

Peptide 5.2 (17 aa)

QMKDIFYSLASLAACK (biotin)

Clone D5

PLYGGIHL~~Y~~PGTMGVPGFP~~RQ~~VKVLGDPADKNFYDWEM

Peptide 5.3 (14 aa)

ADKNFYDWEMAACK (biotin)

Clone A6

YRGMLV~~L~~GRISDGAGKVASPPARIQKVFAVNFYDWEMV

Peptide 5.4 (12 aa)

SAKNFYDWEMVKK (biotin)

FIGURE 21



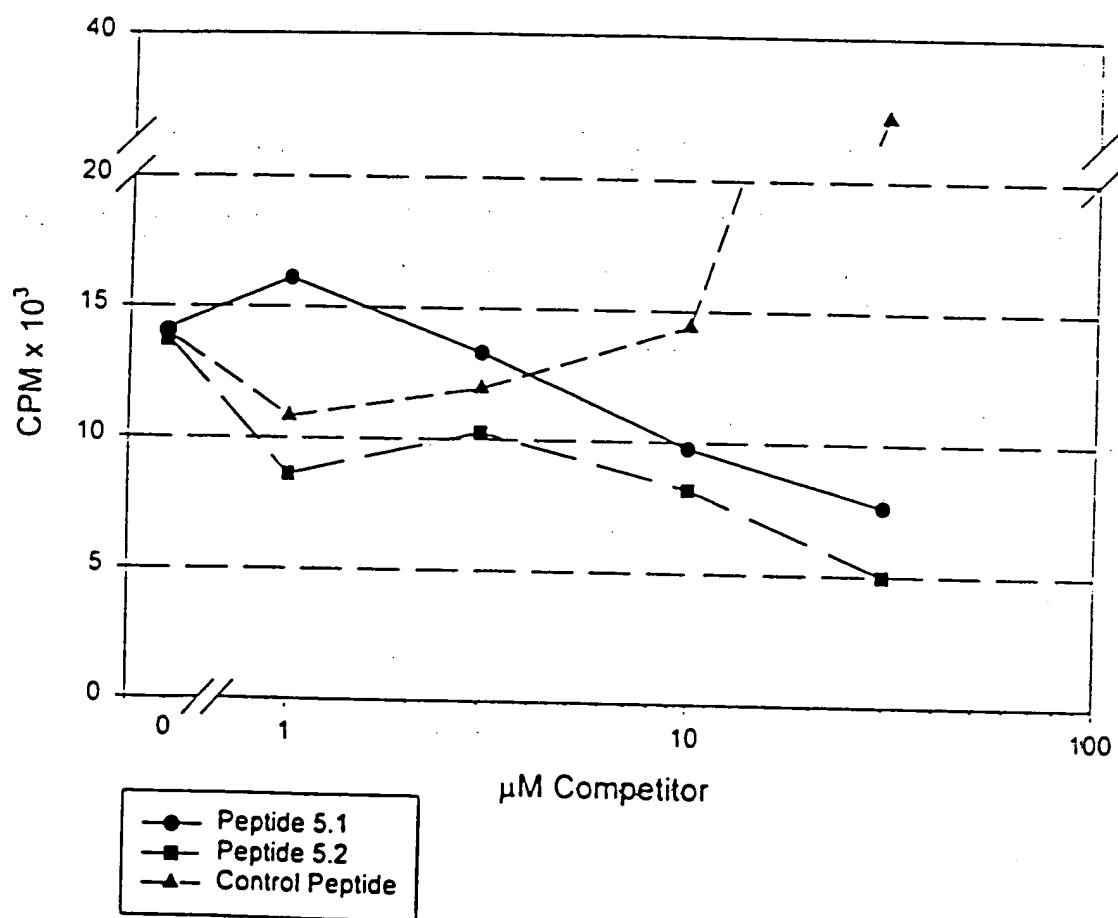


FIGURE 22



Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
B6C-3-C4-IGFR	EHMNTVDPEFYHKLSELLRESGA	--	--	--	--	--	--
B6C-3-F5-IGFR	EHMNTVDPEFYHKLMTELLRESGA	21.0	23.1	--	--	--	--
B6C-3-D4-IGFR	EHMNTVDPEFYHKLSELLRESGA	26.5	22.6	--	--	--	--
B6C-3-A3-IGFR	EHMNTVDPEFYHKLSELLRESGA	26.6	22.1	--	--	--	--
B6C-3-C9-IGFR	EHMNTVDPEFYQKLSSELLRESGA	29.7	20.8	--	--	--	--
B6C-3-C8-IGFR	EHMNTVDPEFYHKLSELLRESGA	29.6	20.5	--	--	--	--
B6C-3-A8-IGFR	EHMNTVDPEFYQRLFELLRESGA	30.5	19.9	--	--	--	--
B6C-3-A2-IGFR	EHMNTVDPEFYHGLQELLRESGA	29.7	19.7	--	--	--	--
B6C-3-C10-IGFR	EHMNTVDPEFYHRLSELLRESGA	33.6	19.0	--	--	--	--
B6C-3-F7-IGFR	EHMNTVDPEFYHNLSELLRESGA	33.0	18.3	--	--	--	--
B6C-3-F10-IGFR	EHMNTVDPEFYQKLSSELLRESGA	30.0	17.7	--	--	--	--
B6C-3-C12-IGFR	EHMNTVDPEFYQKLSSELLRESSA	27.3	17.6	--	--	--	--
B6C-3-E11-IGFR	EHMNTVDPEFYHKLSELLRESGA	27.4	17.4	--	--	--	--
B6C-3-F8-IGFR	EHMNTVDPEFYHKLSELLRESGA	28.4	17.3	--	--	--	--
B6C-3-F2-IGFR	EHMNTVDPEFYHKLSELLRESGA	28.0	17.2	--	--	--	--
B6C-3-D5-IGFR	EHMNTVDPEFYHKLSELLRESGA	25.4	16.0	--	--	--	--
B6C-3-A4-IGFR	EHMNTVDPEFYHKLSELLRESGA	30.8	15.1	--	--	--	--
B6C-3-D3-IGFR	EHMNTVDPEFYHKLSELLRESGA	2.9	14.7	--	--	--	--
B6C-3-F9-IGFR	EHMNTVDPEFYHKLSELLRESGA	2.4	14.3	--	--	--	--
B6C-3-A7-IGFR	EHMNTVDPEFYHKLSELLRESGA	22.6	13.9	--	--	--	--
B6C-3-H10-IGFR	EHMNTVDPEFYHKLSELLRESGA	28.0	13.8	--	--	--	--
B6C-3-A1E-IGFR	EHMNTVDPEFYHKLSELLRESGA	24.8	13.6	--	--	--	--
B6C-3-E12-IGFR	EHMNTVDPEFYHKLSELLRESGA	14.4	12.8	--	--	--	--
B6C-3-H12-IGFR	EHMNTVDPEFYHKLSELLRESGA	17.1	11.1	--	--	--	--
B6C-3-G1-IGFR	EHMNTVDPEFYHKLSELLRESGA	2.3	11.0	--	--	--	--
	EHMNTVDPEFYHKLSELLRESGA	23.3	10.5	--	--	--	--
	EHMNTVDPEFYHKLSELLRESGA	2.7	10.1	--	--	--	--
	EHMNTVDPEFYHKLSELLRESGA	2.3	9.9	--	--	--	--
	EHMNTVDPEFYHKLSELLRESGA	--	--	--	--	--	--

FIGURE 2K

Clone	Sequence
Design	XXXXXXXXFYDAIDQLVXXXXXX
Parental	FYDAIDQLVRSARAGGTRD
20E2A-4-F9-IR	PPWGARFYDAIEQLVFPDNLCC
20E2A-4-E2-IR	IGRVRSFYDAIDQLFQSDMER
20E2A-3-B6-IR	RDAGSSFYDAIDQLVCLTYFC
20E2A-3-A7-IR	MPMGLNFYDIEQLVREWGDD
20E2A-4-F7-IR	TISAHTFYEAITYQLIEGIDPL
20E2A-3-C9-IR	SPWGRAFYDALDQLMGAERG
20E2A-3-C11-IR	LSPPRDFYDAIQQLVVDGWWG
20E2A-4-G7-IR	HGVPRTFYDAIDQLVWGIEVG
20E2A-4-H11-IR	GGTDQLFYGAIDQLVGGTWMR
20E2A-4-E9-IR	LSVHQSFYDAINELIFSGLEA
20E2A-4-F4-IR	GDARDPFYDAMEQLVYGELGG
20E2A-3-A3-IR	VASPRSFEAIAQLVFNLGQE
20E2A-4-E4-IR	RKPCQTFYDCIIDLVTVDV
20E2A-4-G5-IR	LLSRWTFYDAIEQLVGGADG
20E2A-4-H1-IR	PAGCQGFYEAEQLVTGECG
20E2A-3-D8-IR	AVFPRTFEAIDQLVGVSLLG
20E2A-4-F11-IR	APIPFSEFYDAIVQLVMQGDHE
20E2A-3-C1-IR	QCNPRTFEAIAQLVTGCDVS
20E2A-3-B2-IR	VSTSGSFYDAIQQLLEDSWGW
20E2A-4-G10-IR	HHSAFSEFYDAIAQLVGVPMEE
20E2A-3-A5-IR	FTYVHSFYDAIEQLVRGEGGG
20E2A-4-H3-IR	QGNANFYDAIDQLCFGCLGG
20E2A-3-C4-IR	SSEGWTFYDAIDQLVGRERGM
20E2A-4-E3-IR	PDGCATFYHAIQQLVTGFPV
20E2A-4-E7-IR	RGPMTFYDAIAQLVAQSADG

Ratios over Background				Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
--	--	--	--	--	--
30.6	15.1	4.2	3.6	0.3	
19.9	1.2	13.9	0.1	11.5	
13.9	1.3	9.7	0.1	7.6	
14.5	1.6	6.1	0.3	3.8	
18.6	4.2	15.2	0.3	3.6	
20.1	10.6	15.8	0.7	1.5	
24.4	16.4	23.8	0.7	1.4	
14.8	5.9	6.6	0.9	1.1	
17.2	8.3	8.9	0.9	1.1	
25.4	26.9	25.6	1.1	1.0	
4.7	2.1	2.1	1.0	1.0	
12.6	5.6	5.7	1.0	1.0	
21.0	11.9	12.1	1.0	1.0	
21.0	16.0	16.1	1.0	1.0	
22.1	19.5	18.8	1.0	1.0	
24.4	20.4	21.2	1.0	1.0	
22.3	20.8	20.3	1.0	1.0	
23.2	21.0	20.4	1.0	1.0	
23.4	22.3	22.5	1.0	1.0	
24.6	22.5	22.8	1.0	1.0	
21.5	22.9	22.2	1.0	1.0	
24.6	23.4	22.6	1.0	1.0	
24.5	24.1	25.1	1.0	1.0	
25.2	24.4	24.7	1.0	1.0	
18.5	15.7	13.6	1.2	0.9	
17.8	16.6	14.4	1.2	0.9	

FIGURE 2L





Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	ICFR	IR	ICFR/IR	IR/ICFR
20E2A-3-B3-IR	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--
20E2A-3-B3-IR	RSSCQSFYDAIERLVLCGTCG	22.4	18.6	15.9	1.2	0.9
20E2A-4-H10-IR	VSRRKFSFYDAIQQLVVRGDAGV	24.8	24.5	21.2	1.2	0.9
20E2A-4-F8-IR	FQRTWSFYDAINQLVMEGSGD	4.3	2.2	2.1	1.1	0.9
20E2A-4-H5-IR	RGSATTFYDAINQLVGGQDGCW	21.3	18.3	16.5	1.1	0.9
20E2A-4-G1-IR	AQPCVSFYDAIEQLVTRGSCM	21.4	18.3	16.0	1.1	0.9
20E2A-4-F2-IR	GGDGPFFYDWMIEQLVRAGSEA	20.1	20.5	18.2	1.1	0.9
20E2A-4-H7-IR	LDLCA SFYDAIEQLVGKFCG	22.6	21.2	18.6	1.1	0.9
20E2A-3-D5-IR	WLACQSFYDAIDQLINGECN	22.7	21.3	18.9	1.1	0.9
20E2A-3-A1-IR	EVNALSFYDAIDQLVRRGLGG	23.8	21.7	19.9	1.1	0.9
20E2A-4-H9-IR	RLQPRTFYDAIDQLIGVLEG	24.0	22.5	20.8	1.1	0.9
20E2A-3-D7-IR	SGAHRTFYDAIQELVGMGSK	24.1	23.5	21.0	1.1	0.9
20E2A-4-E5-IR	NMQSLTFYDAIAQLVLRSGG	24.1	23.5	20.9	1.1	0.9
20E2A-4-E11-IR	RAVGATFYDQINQLVRKDDGY	22.5	14.6	11.7	1.3	0.8
20E2A-3-A4-IR	SQCRGGFYDAIYQLVTGVNCI	20.2	17.5	13.4	1.3	0.8
20E2A-4-G8-IR	DRLAFSFYDAIDQLVHCCGHG	21.7	18.0	13.8	1.3	0.8
20E2A-3-B7-IR	GNRQRGFYDAIDQLVGGSWWR	21.1	21.4	16.9	1.3	0.8
20E2A-4-G11-IR	GGSVLSFYDAIAQLVGGQSI	22.9	23.1	17.7	1.3	0.8
20E2A-3-C5-IR	RSGPMSFYDAIEQLVGRLLHP	24.2	24.3	19.0	1.3	0.8
20E2A-4-E8-IR	VSGCRTFYDAIDQLVSGQACG	17.1	11.5	9.4	1.2	0.8
20E2A-4-H2-IR	AQFPRTFYDAIEQLVHGKMD	21.6	13.7	11.6	1.2	0.8
20E2A-4-H4-IR	CAQPE SFYDAIDRLVTGRCLV	21.3	19.6	16.3	1.2	0.8
20E2A-3-D4-IR	PDECQSFYCAIDRLVTGKGR	23.2	22.2	18.0	1.2	0.8
20E2A-4-F5-IR	QRRARDFYEAIQQLVGVAGL	12.2	5.7	3.8	1.5	0.7
20E2A-3-B10-IR	PLVRGTFYDAIKQLVMSGSSD	14.9	5.9	3.9	1.5	0.7
20E2A-3-B9-IR	VGIAMTFYDAIQQLVGRSPEG	15.5	11.0	7.2	1.5	0.7
20E2A-3-D10-IR	PRGQASFYDMEQLVGSADWN	22.2	19.1	12.8	1.5	0.7
20E2A-3-D6-IR	DGRVMSFYDAIEQLVGQFECP	21.8	19.3	13.0	1.5	0.7
20E2A-4-G9-IR	RFVVR SFYDAIEQLILAPNLC	21.3	19.9	13.3	1.5	0.7
20E2A-4-E1-IR	KVGRGSFYDAIRELVGGQGHV	23.1	20.7	13.6	1.5	0.7
20E2A-4-F12-IR	PAIGFTFYDAIRQLVWFOGAD	17.5	17.1	12.1	1.4	0.7
20E2A-4-G3-IR	ALPGRSFYDAIAQLVGPDMGA	21.6	19.4	14.1	1.4	0.7

FIGURE 2L (Con't)



Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFSR	IR	IGFI/IR	IR/IGFI	
20E2A-3-C2-IR	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--	--
20E2A-3-B1-IR	RPQGGTFYDMIKQLVLGSGWG	23.4	20.9	15.4	1.4	0.7	
20E2A-3-A8-IR	WSAFADFYDAIQHLVAGEVGA	22.1	21.6	15.6	1.4	0.7	
20E2A-3-A8-IR	SDGRDGFYDAIQQLVRSAFCD	12.3	4.8	2.7	1.8	0.6	
20E2A-4-C2-IR	IRSVFSFYDAIDQLVKGKGS	18.9	13.8	7.9	1.8	0.6	
20E2A-3-A9-IR	GGVSLTFYEAIQQLVRCGFDA	23.3	20.3	11.3	1.8	0.6	
20E2A-3-D3-IR	AAQAFSFDLINQLVASKPSE	24.4	24.5	13.5	1.8	0.6	
20E2A-3-A11-IR	QSGACGFYDAINQLVGSIC	13.5	4.6	2.7	1.7	0.6	
20E2A-3-B4-IR	GGIVFSFYDAIDQLVRCNGAG	21.4	15.3	8.9	1.7	0.6	
20E2A-4-E10-IR	IYTGQGFYDAIEQLVRCGSTP	22.3	19.0	11.3	1.7	0.6	
20E2A-3-D2-IR	KSPALSFYDAIEQLVGSQGVK	22.5	19.0	11.2	1.7	0.6	
20E2A-4-F1-IR	ISPPWTFYDAIDQLVGSDDGR	14.5	6.2	3.9	1.6	0.6	
20E2A-3-D1-IR	GSRRFGFYDAIDQLVRQGCLE	16.5	6.6	4.0	1.6	0.6	
20E2A-3-D11-IR	GVAGGTFYDAIEQLVRQFGCS	20.2	14.4	8.9	1.6	0.6	
20E2A-3-C3-IR	RPLRWSFYDALDQLVGSALICG	23.9	22.5	14.2	1.6	0.6	
20E2A-3-C12-IR	MQGRGGFYDAIADLVGCHVRG	21.3	23.0	14.4	1.6	0.6	
20E2A-3-A2-IR	TSQGLSFYDAINQLVAGCWG	18.9	11.6	7.5	1.5	0.6	
20E2A-3-C7-IR	SGGTVTFYDAINQLVQGRYNG	21.6	15.1	6.9	2.2	0.5	
20E2A-3-C10-IR	GGALDPFYDAIYQLVIRGSSG	18.1	18.0	9.1	2.0	0.5	
20E2A-3-D9-IR	KQRGVTFYDLNQLVGSARG	21.8	21.6	8.4	2.6	0.4	
20E2A-3-B5-IR	PRAPRSFYDAIHQLVGRQCPG	24.3	18.1	7.4	2.5	0.4	
20E2A-3-A6-IR	PCSDDQFYDALSQLVGIRVCP	17.8	19.1	7.6	2.5	0.4	
20E2A-4-G12-IR	SYGYQSFYDAIEELVRCPPAR	9.0	9.3	2.6	3.6	0.3	

FIGURE 2L (Con't)



Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Targ	IGFsk	IR	IGF/IR	IR/IGF	
Parental	XXXXXXXXFYDAIDQLVXXXXXX	--	--	--	--	--	--
20E2A-4-F11-IGFR	FYDAIDQLVGRSARAGSTRD	30.6	15.1	4.2	3.6	0.3	
20E2A-4-F12-IGFR	QCGSASFYDAIDRLRMIRIGG	21.3	18.8	1.3	14.6	0.1	
20E2A-3-B4-IGFR	AQCGSEFYDALAQVLVQGVSG	23.3	23.9	3.1	7.8	0.1	
20E2A-4-F4-IGFR	GHPAVSFYDAIDQLRRRCGG	21.8	16.6	2.4	6.9	0.1	
20E2A-3-C7-IGFR	YSDTYSFYDAIVQLVRCGASA	20.7	20.0	3.6	5.5	0.2	
20E2A-3-C10-IGFR	VGTVAGFYDAIAQLVARASRV	17.6	5.4	1.1	5.1	0.2	
20E2A-3-D6-IGFR	RFVWGSFYDAIDQLVGRWRG	23.3	21.0	4.2	5.0	0.2	
20E2A-4-F6-IGFR	RAVGDSFYEAIDQLVGRGHV	15.1	11.8	2.4	5.0	0.2	
20E2A-3-A8-IGFR	LRSQLSFYEAIDQLVQWKGA	21.5	19.9	4.3	4.6	0.2	
20E2A-4-F9-IGFR	DKFSTSFYDAIDQLVQSVRGV	22.2	13.3	2.9	4.6	0.2	
20E2A-3-F3-IGFR	MQSGFSFYDAIDRLVGRIGER	21.2	19.0	4.4	4.4	0.2	
20E2A-4-B2-IGFR	VGSSSFYEAIERLVQGLGRH	20.6	19.3	4.6	4.2	0.2	
20E2A-3-D10-IGFR	LSWAGFYEAIDQLVRSQGRH	18.7	14.7	3.8	3.9	0.3	
20E2A-4-G8-IGFR	QOVHAGFYEALEELVGFGLG	20.9	10.8	2.7	3.9	0.3	
20E2A-3-A12-IGFR	LSVALSFYDALGQLVAGGGRW	20.6	6.9	1.8	3.9	0.3	
20E2A-4-H1-IGFR	SGSNLGFYDALRQLVGCATDGS	16.1	4.3	1.1	3.9	0.3	
20E2A-3-D7-IGFR	PSGFLSFYEAIIDQLVHGVRF	17.8	9.7	2.6	3.7	0.3	
20E2A-4-A9-IGFR	AFTPTSFYDAIEQLVQQLSPR	20.8	14.5	4.1	3.5	0.3	
20E2A-3-B11-IGFR	VSSLRSFYDALDELVRPFOQ	19.5	17.9	5.3	3.4	0.3	
20E2A-4-H5-IGFR	IGVSRGFYDAIDKLVRDRGSP	22.0	18.3	5.6	3.3	0.3	
20E2A-3-D12-IGFR	GRLSLSFYDLIDQLVQAGNGG	24.7	10.5	3.2	3.3	0.3	
20E2A-4-H11-IGFR	GQRAQSFYEALARLVCEGRCT	26.3	15.4	4.8	3.2	0.3	
20E2A-4-E11-IGFR	CRFQGSFYDAIDLLVLCVRTC	15.8	10.7	3.4	3.2	0.3	
	RWAFQSFYDAIDHLVNHREGH	13.9	9.0	2.8	3.2	0.3	
	LPSSSGFYNAIQQLVCGHRCG	22.8	17.5	5.7	3.1	0.3	
		20.1	16.6	5.5	3.0	0.3	
		21.0	12.6	4.2	3.0	0.3	

FIGURE 2M



Clone Design	Sequence
20E2A-4-F2-IGFR	XXXXXXXXFYDAIDQLVXXXXXX
20E2A-3-D4-IGFR	TGVFNDFYDALQQLVGFVRVD
20E2A-3-B1Q-IGFR	YGSFETFYDAIDQLVRRGSQP
20E2A-4-E5-IGFR	ROLDSFYDAIDQLVRRSESRP
20E2A-3-D5-IGFR	WPRGDPFYDAMEKLLSQGGGR
20E2A-4-G11-IGFR	PGLIQSFYDAIDQLVRQGRGN
20E2A-3-C12-IGFR	MNVFSFYDAIDQLVCGQRIGC
20E2A-4-G5-IGFR	LDMIGFYDAIDQLVSGSLAP
20E2A-3-D9-IGFR	RRPCNSFYDAIDQLLVGGPCG
20E2A-4-F10-IGFR	FGRRSTFYDLIDQLVGQGRGT
20E2A-4-E2-IGFR	LRAPRSFYDAIYQLAQRPSPV
20E2A-4-E3-IGFR	VQRFSSFYDALDQLVGHGVWK
20E2A-3-C4-IGFR	PSARMGFYDLIDQLVGLVPGS
20E2A-3-C5-IGFR	SLQPHDFYDAIHRLVFHGGRF
20E2A-4-G12-IGFR	ERHGSFYDAIAQLQSDRSR
20E2A-3-C3-IGFR	YQPPGSFYDWIRELVAGPRE
20E2A-3-B7-IGFR	FAHASSFYDAIDQLVAKQSP
20E2A-4-E10-IGFR	AQSSSGFYDALYQLVWGRGPG
20E2A-4-E6-IGFR	TTSGGSFYDAMYQLVWCDWRR
20E2A-3-D3-IGFR	ARGTAGFYAELERLVRCQDHG
20E2A-4-G4-IGFR	PRHAINFYDAIHQLVFGPRQ
20E2A-4-F1-IGFR	QSAHWSFYDAIERLVNMDTMP
20E2A-4-H7-IGFR	VGVVSSFYDAIDQLVGMWRGS
20E2A-3-B9-IGFR	DTLIASFYDAIDQLVRLGRNQ
20E2A-4-E9-IGFR	FQGTQGFYDAIERLMRRGERP
20E2A-3-B1-IGFR	WADWGSFYDAIEQLVQRGCGV
20E2A-4-G1-IGFR	EQLSGCFYDAIHQLVHGGGLG
20E2A-4-E7-IGFR	CGQRCSFYDAIDQLVGLPGA
20E2A-3-D11-IGFR	MMRVDFYDAIDRLVNEGAT
20E2A-3-A3-IGFR	RGQATSFYDAIDQLVMGSGCV
20E2A-4-G7-IGFR	GHYFGSFYDAIDQLVAGMLPG
	PEGVQGFYDALAHLVGSLLFC

Ratios over Background				Comparisons	
E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
--	--	--	--	--	--
19.4	19.0	6.8	2.8	0.4	
16.1	11.8	4.2	2.8	0.4	
24.0	14.3	5.3	2.7	0.4	
18.1	20.6	7.9	2.6	0.4	
15.1	9.3	3.6	2.6	0.4	
20.7	3.3	1.3	2.6	0.4	
25.9	17.4	7.2	2.4	0.4	
23.6	14.6	6.0	2.4	0.4	
19.8	12.3	5.1	2.4	0.4	
21.4	21.6	9.3	2.3	0.4	
22.6	21.3	9.1	2.3	0.4	
21.0	21.8	10.1	2.2	0.5	
23.5	17.4	7.8	2.2	0.4	
22.2	17.1	7.7	2.2	0.4	
24.3	16.3	7.4	2.2	0.5	
11.3	2.7	1.2	2.2	0.5	
22.3	22.6	10.8	2.1	0.5	
22.6	19.9	9.4	2.1	0.5	
23.0	16.6	7.9	2.1	0.5	
20.5	15.7	7.6	2.1	0.5	
22.6	14.5	7.0	2.1	0.5	
19.6	19.9	9.8	2.0	0.5	
23.0	17.1	8.7	2.0	0.5	
26.4	22.1	11.5	1.9	0.5	
25.3	20.7	11.1	1.9	0.5	
23.1	17.9	9.5	1.9	0.5	
22.6	17.7	9.3	1.9	0.5	
17.2	8.6	4.6	1.9	0.5	
16.1	6.1	3.2	1.9	0.5	
5.2	3.0	1.5	1.9	0.5	
24.4	21.1	11.5	1.8	0.5	

FIGURE 2M (Con't)



Clone	Sequence
Design	XXXXXXXXFYDAIDQLVXXXXXX
20E2A-4-G2-IGFR	IGVLGSFYDAIDQLVRQGNR
20E2A-4-G3-IGFR	RDVADGFYAAIEQLVRGQFGL
20E2A-3-B5-IGFR	VRQAKSFYDAIDQLVRGALRG
20E2A-4-H4-IGFR	QVFRGSFYDAIDALVRMGRA
20E2A-4-F8-IGFR	VGAAFSFYDAIDQLVGMSPGS
20E2A-3-A6-IGFR	PSPVMSFYDAIQQLVRSQORG
20E2A-4-H12-IGFR	PVSATSFYDAINQLVRMGRG
20E2A-3-B12-IGFR	VMRRDRFYDAIEQLVGRIGV
20E2A-3-B8-IGFR	TTYVNSFYDALQQLVGGRIGV
20E2A-3-C8-IGFR	LSNMTFYDAINQLVGHVQSL
20E2A-4-H10-IGFR	ASSRLSFYDAIEQLIKWSPGP
20E2A-3-C9-IGFR	WDLVDSFYDAIDQLVGRVPG
20E2A-4-H2-IGFR	FAFVGSFYDALQQLVAGPPRS
20E2A-3-B6-IGFR	EDQPN SFYDAIRQLVMGRSLP
20E2A-4-G9-IGFR	SVGPRSFYDAIDQLVGAWVG
20E2A-4-H6-IGFR	KFRVYTFYDAIDQLVNOGRGR
20E2A-4-H9-IGFR	GRGWGSFYEAIDQLVRLGET
20E2A-4-G10-IGFR	FTSFHTFYDAIEQLVQGQDGP
20E2A-3-A4-IGFR	AGSVTSFYDAMEQLVATGTS
20E2A-3-A7-IGFR	PRESFSFYDAIHQLVTGRVRS
20E2A-4-E12-IGFR	LGRADGFYDAIKQLVGADWGC
20E2A-3-D1-IGFR	RSGTWTFYDALEQLVQSGSR
20E2A-3-C6-IGFR	PVVLFSFYDAIDQLVRKGLGP
20E2A-3-D2-IGFR	GRRAQTFYDALEQLVGEALG
20E2A-4-E8-IGFR	AGPDMSFYDAIDQLVHCCGPF
20E2A-4-G6-IGFR	HGEKLSFYDAIAQLVGFDIGH
20E2A-4-F5-IGFR	GYTPVD FYDAIRQLVTGWPFG
20E2A-3-C2-IGFR	FGGFSSFYDALDQLVLRGRSD
20E2A-4-H8-IGFR	VGIVRGFYEAIERLVGDTHGQ
20E2A-3-A5-IGFR	TPGGFSFYDAIQQLVDVLSDS
20E2A-3-C11-IGFR	TNALTFYDAIEQLVRWGQRD

Ratios over Background				Comparisons	
E-Tag	IGFSR	IR	IGFSR	IR/IGFSR	IR/IGFSR
--	--	--	--	--	--
22.3	17.5	9.9	1.8	0.6	0.6
21.2	12.3	6.9	1.8	0.6	0.6
24.0	22.7	13.3	1.7	0.6	0.6
22.2	20.6	12.0	1.7	0.6	0.6
17.3	17.9	10.7	1.7	0.6	0.6
23.8	23.7	15.0	1.6	0.6	0.6
25.1	23.5	14.2	1.6	0.6	0.6
27.6	21.9	13.6	1.6	0.6	0.6
21.5	19.0	12.2	1.6	0.6	0.6
23.2	17.7	11.4	1.6	0.6	0.6
25.3	23.8	16.2	1.5	0.7	0.7
25.4	21.8	14.6	1.5	0.7	0.7
21.8	20.1	13.0	1.5	0.7	0.7
20.3	18.1	11.8	1.5	0.7	0.7
26.0	16.1	10.8	1.5	0.7	0.7
21.9	19.6	13.9	1.4	0.7	0.7
24.9	16.8	11.8	1.4	0.7	0.7
25.3	16.5	12.1	1.4	0.7	0.7
16.8	2.5	1.8	1.4	0.7	0.7
26.0	24.9	19.3	1.3	0.8	0.8
23.3	23.1	17.8	1.3	0.8	0.8
24.0	22.4	17.6	1.3	0.8	0.8
23.7	21.7	17.2	1.3	0.8	0.8
21.4	15.1	11.4	1.3	0.8	0.8
18.4	13.6	10.4	1.3	0.8	0.8
24.7	21.9	17.7	1.2	0.8	0.8
21.7	21.7	18.2	1.2	0.8	0.8
22.5	19.6	15.8	1.2	0.8	0.8
24.4	18.5	15.1	1.2	0.8	0.8
22.7	15.6	12.6	1.2	0.8	0.8
25.8	24.3	21.2	1.1	0.9	0.9

FIGURE 2M (Con't)



Clone
Design
20E2A-3-C1-IGFR
20E2A-3-B3-IGFR
20E2A-3-D8-IGFR

Sequence
XXXXXXXXFYDAIDQLVXXXXXX
GQSPLSFYDAIDQLVRAFPVG
AGQLCGFYIAICQLVGYEYCT
SAGPLSFYDAIAQLVGPWRL

Ratios over Background				Comparisons	
E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
--	--	--	--	--	--
23.4	22.4	20.5	1.1	0.9	
21.0	17.0	14.8	1.1	0.9	
22.0	19.7	19.6	1.0	1.0	

FIGURE 2M (Cont'd)

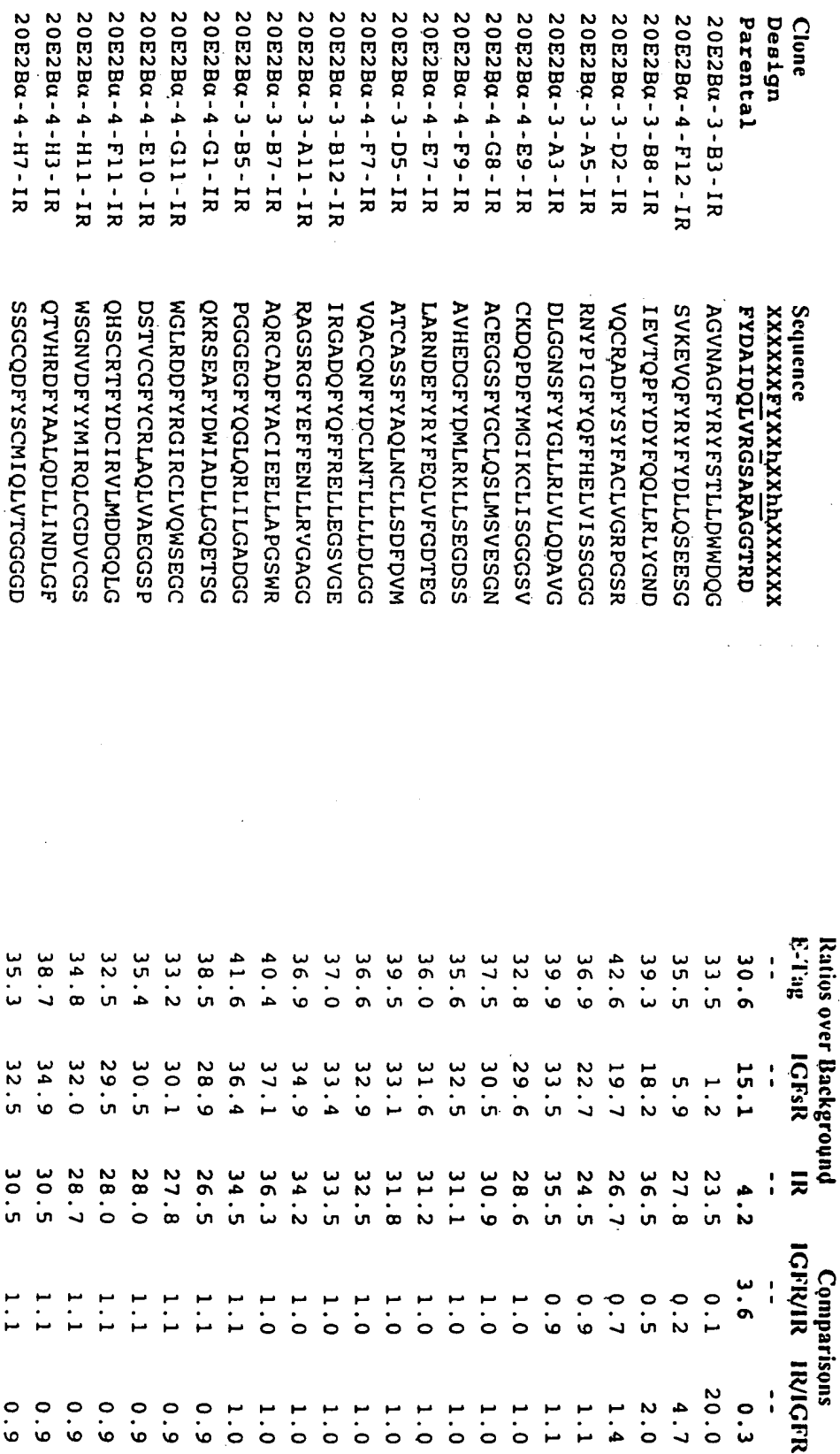


FIGURE 2N

Clone	Sequence	Ratios over Background		Comparisons	
Design	xxxxxxfyxxhxxhxxxxxx	E-Tag	IGFR	IR	IGFR/IR IR/IGFR
20E2Bq-3-B6-IR	SGPMVGFYRGLFSLSPEDLQ	39.7	34.9	31.5	1.1 0.9
20E2Bq-3-D1-IR	LAEPDSFYMWIAQLLEEFAG	41.6	35.1	31.7	1.1 0.9
20E2Bq-3-A9-IR	FSGCDNFYSCLQSLWLPGCV	37.3	35.1	32.4	1.1 0.9
20E2Bq-3-C4-IR	QVFCDNFYHCIELLGVGQTP	39.6	36.3	33.4	1.1 0.9
20E2Bq-4-F3-IR	RGRDNQFYHGLMALLGSGLE	37.5	36.6	33.6	1.1 0.9
20E2Bq-4-F4-IR	VSGRGGFYDAIRDLIGPRDQG	37.2	36.9	33.7	1.1 0.9
20E2Bq-3-D4-IR	PVVLDDFYVALCQLMVOGDCF	42.1	38.0	34.5	1.1 0.9
20E2Bq-4-E4-IR	PDIADPFYAFFQGLLRADTPI	40.6	38.4	35.5	1.1 0.9
20E2Bq-4-G10-IR	VAQCTDFYACIRSLVRSRSGPG	32.9	31.3	27.1	1.2 0.9
20E2Bq-3-D11-IR	CSQLVSFYLGMDCLLGRGCTQ	34.0	32.5	27.9	1.2 0.9
20E2Bq-3-C8-IR	PLACADFYQCLSDLIRGGPAW	39.2	33.0	28.2	1.2 0.9
20E2Bq-4-F2-IR	VVICTGFYDCIYQLVGSHEEM	38.7	37.6	32.3	1.2 0.9
20E2Bq-4-H12-IR	CVDRRTFYEGLQCLLGATGD	32.3	30.4	25.8	1.2 0.8
20E2Bq-4-E1-IR	VNLRDPFYQWIEALMDSAGGE	39.2	40.2	32.3	1.2 0.8
20E2Bq-4-H8-IR	LTSSTSFYDALFCLAGLQLCG	37.6	34.8	27.0	1.3 0.8
20E2Bq-3-B4-IR	DFDSSPFYRGLRQLLESRSFP	39.9	34.9	25.9	1.3 0.7
20E2Bq-4-E2-IR	HEAGWTFYDAIQCLVGWCSK	38.8	36.3	23.5	1.5 0.6
20E2Bq-4-H1-IR	CQQWRSFYHAVSCLLGPDDPD	40.8	33.6	20.2	1.7 0.6
20E2Bq-3-A10-IR	MVDRDPFYQGLRDLIGRQKEG	32.8	32.6	18.5	1.8 0.6
20E2Bq-3-D3-IR	LGRRGGFYRGLQDLIGTQMPR	41.9	29.5	5.6	5.3 0.2

FIGURE 2N (Cont.)



Clone	Sequence	Ratios over Background		Comparisons	
Design	xxxxxxffxxhxxhxxxxxx	E-Tag	ICFR	IR	ICFR/IR IR/ICFR
20E2Bf-4-F7-IR	DALNLRfYsYfQhLMEDQVTD	26.8	3.0	24.2	0.1 8.0
20E2Bf-3-E12-IR	GNSGGSfYRfYfQhLLDSDGMS	17.2	1.4	5.5	0.3 4.0
20E2Bf-4-F3-IR	GDRVPGFYDwIRQhLMVDPLEV	25.2	2.0	7.7	0.3 3.9
20E2Bf-4-F6-IR	SEREDPfYRwIQhMVEGVSEG	25.7	3.8	11.0	0.4 2.9
20E2Bf-3-D11-IR	GSVACDFYCHMwSLVEQPAQT	14.8	3.6	4.2	0.9 1.2
20E2Bf-3-E5-IR	VHPSAGfYKGLLALIGDSQLG	24.3	6.9	4.3	1.6 0.6
20E2Bf-3-C9-IR	PCGGLSFYGGCLQhELLTWESPT	29.7	24.3	15.0	1.6 0.6
20E2Bf-3-C7-IR	QSGSGDFYDwLSRLIRGNGDG	1.5	3.1	1.5	2.0 0.5
20E2Bf-4-H8-IR	LPRQDGFYDALRRLISEGAGG	25.8	26.9	13.2	2.0 0.5
20E2Bf-4-G7-IR	LQPCSGfYECIERLIGVKLSG	19.9	25.2	1.6	15.8 0.1

FIGURE 2N (Con't)





Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
20E2B-1-A6-IGFR	XXXXXXXXFYXXhxxhXXXXXXXX	18.6	18.1	1.1	16.8	0.1	
20E2B-3-C6-IGFR	GVRAMSFYDALVSVLGLGPSG	17.9	16.8	1.1	14.8	0.1	
20E2B-4-H3-IGFR	VEGRGLFYDRLRLRLARRQNG	11.2	14.8	1.1	13.9	0.1	
20E2B-3-C2-IGFR	KLHNLMFYGLRLVWGAGLG	13.1	8.9	0.6	13.8	0.1	
20E2B-3-E3-IGFR	GNGDGMFYQLSLVGRDMHV	22.4	16.3	1.3	13.1	0.1	
20E2B-4-H12-IGFR	PDLHKGFYAQLAQLIRGQLLS	6.5	9.7	0.8	12.8	0.1	
20E2B-3-D2-IGFR	YSCGDGFYSLSLSDLLGGQFRC	20.7	12.4	1.1	11.7	0.1	
20E2B-3-D8-IGFR	IQQLTFYDRLRLVRSLELGS	20.4	17.7	1.6	11.3	0.1	
20E2B-3-E8-IGFR	GGTEVDFYRALERLVRGQLGL	15.7	16.7	1.5	11.1	0.1	
20E2B-4-F8-IGFR	LRIANLFYQRLMDLAFGGGG	12.3	7.3	0.8	9.7	0.1	
20E2B-1-A11-IGFR	PVGVOGFYEGLSRLVLGRGWM	15.0	9.5	1.0	9.7	0.1	
20E2B-3-D4-IGFR	RFSTDGFYQYLALVGGGPVG	8.1	7.9	0.8	9.6	0.1	
20E2B-2-B11-IGFR	NSRDGFFYLQLERLLGFPVVG	13.9	10.6	1.1	9.4	0.1	
20E2B-3-C8-IGFR	VVTPVNFYRALVALVRGQRLG	18.5	15.6	1.8	8.9	0.1	
20E2B-2-B2-IGFR	QPADGFFYSALMKLIGRGVS	11.7	4.9	0.6	8.1	0.1	
20E2B-4-F10-IGFR	PGTDLGFYQALRCVVIQACD	19.0	17.3	2.2	7.8	0.1	
20E2B-3-D11-IGFR	AQPCGFFYGLLEQLVGRSVCD	11.9	14.7	1.9	7.7	0.1	
20E2B-3-C11-IGFR	QPDHSYFYSLLQELVGSFEERL	14.3	12.2	1.6	7.6	0.1	
20E2B-2-B3-IGFR	LGVTDFYALGYLHGVGQF	15.3	15.4	2.1	7.5	0.1	
20E2B-3-D12-IGFR	CMMDGFYAGLCLLTAGEGR	9.1	5.3	0.7	7.4	0.1	
20E2B-2-B8-IGFR	ICTGGFYQVLCGLRGT SAR	10.3	6.2	0.9	7.3	0.1	
20E2B-3-E12-IGFR	QGNVLDFFYGMIGRLAKQSD	13.9	6.0	0.8	7.3	0.1	
20E2B-4-G11-IGFR	VATSGFFYSGLSELLOGGGNV	17.4	5.7	0.8	7.2	0.1	
20E2B-3-D6-IGFR	IMATGDFYRLLSQLVMGRVGT	8.9	4.5	0.6	7.0	0.1	
20E2B-2-B7-IGFR	RQGTGSFYLMLEQLLVGARGP	20.7	17.8	2.6	6.9	0.1	
20E2B-3-C4-IGFR	DSVGDNFYQLLESLVGHGVG	18.0	6.1	0.9	6.7	0.1	
	LSSDGQFYRALNLLQGSAGR	23.4	20.4	3.3	6.2	0.2	
	ASSASGFYELLQRLAGLGLEV						

FIGURE 20

Clone	Sequence	Ratios over Background				Comparisons	
Design		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
20E2B-3-D3-IGFR	XXXXXXXXfYXXhXXhXXXXXXXX	21.0	16.1	2.6	6.2	0.2	
20E2B-4-H8-IGFR	CGSRDfYGGIICLLGQKGV	7.2	5.3	0.9	5.9	0.2	
20E2B-3-E9-IGFR	PAGPCGFYCGGLLHGDPSP	14.7	16.2	2.8	5.8	0.2	
20E2B-4-H9-IGFR	QAPQDfYQGLMLHHRDPTM	4.5	5.2	0.9	5.6	0.2	
20E2B-1-A8-IGFR	RCQGTGFYTCIQELIGFGDPD	16.1	4.4	0.9	5.0	0.2	
20E2B-4-H11-IGFR	TLRSPTFYDWLEMLTHGQGG	10.7	11.0	2.3	4.8	0.2	
20E2B-3-C9-IGFR	STHSRAFYDAIAQLVGSVLGP	17.9	19.7	4.2	4.6	0.2	
20E2B-3-E6-IGFR	RQGGGSFYELLGVLGGEVCV	24.5	21.6	4.7	4.6	0.2	
20E2B-4-G8-IGFR	RQASGFYRALHDLMLRTQDY	16.5	7.7	1.9	4.1	0.2	
20E2B-4-H10-IGFR	SRANLFFYMGLSQLLRDNRL	11.1	14.9	3.7	4.1	0.2	
20E2B-3-E7-IGFR	GRALDPFYDQLRDLVARSGG	2.2	2.5	0.8	3.1	0.3	
20E2B-3-C12-IGFR	EASCRFYCGLMALIGGDDQR	14.4	8.8	3.0	3.0	0.3	
20E2B-4-G12-IGFR	QNGCKDFYCLIDNLIRYCPGG	6.2	6.4	2.2	2.9	0.3	
20E2B-3-E4-IGFR	QHSCTFYDCIRVLMDDGQLG	9.6	10.0	3.8	2.6	0.4	
20E2B-2-B4-IGFR	LDSRGRFYDWIKALIGDRDVQ	27.2	23.8	9.1	2.6	0.4	
20E2B-3-C5-IGFR	CQKGDfYAGLVCLLREASQ	24.9	22.3	8.9	2.5	0.4	
	GGSQSfYDVMCMLLQLDPTC	18.6	20.2	8.7	2.3	0.4	
	VESDVSfYEGMLRLVWVGQGG	5.8	2.3	1.0	2.2	0.5	
	ERAGDLfYQWFERLVAGHGLE	6.3	2.0	0.9	2.2	0.5	
	RMPSGSfYQGIYELVTRQGGF						

FIGURE 20 (Con't)



Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
	XXXXXXXXFYRYFXXLLXXXXXXXX	--	--	--	--	--	
NNRPβ-4-G6-IR	RMPNFYGYFESLTLTHFS	10.1	1.9	20.1	0.1	10.6	
NNRPβ-4-F3-IR	HYNAFYEFQVLLAETW	8.6	1.3	13.6	0.1	10.5	
NNRPα-2-C1-IR	EGWDFYSYFSGLLASVT	19.7	2.0	10.9	0.2	5.3	
NNRPα-4-E1-IR	LDRQFYRYFQDLLVGF	11.5	6.5	21.2	0.3	3.2	
NNRPα-3-H6-IR	WGRSFYRYFETLLAQGI	19.1	2.1	6.0	0.3	2.9	
NNRPβ-4-F7-IR	RREGFYHYFQSLDEYG	0.7	0.9	2.3	0.4	2.7	
NNRPα-2-D1-IR	GGGQFYRYFIDMLVLDI	18.4	1.5	3.7	0.4	2.5	
NNRPα-1-A1-IR	PTGPFDRYFARLVMRG	15.2	1.3	3.1	0.4	2.4	
NNRPα-2-C10-IR	RGAFYRYFEGLLSQHN	18.8	3.8	8.8	0.4	2.3	
NNRPα-3-G1-IR	WRDPFYRYFQDLLEGER	18.9	4.2	8.6	0.5	2.1	
NNRPα-4-C3-IR	WGGEFYRYFVQLLSSED	17.9	12.9	25.7	0.5	2.0	
NNRPα-4-D1-IR	GRESFYGYFLDLLQETV	16.2	12.7	23.2	0.5	1.8	
NNRPβ-4-F4-IR	GHAFFYGYFQGLDSYL	19.5	16.0	25.6	0.6	1.6	
NNRPα-1-B2-IR	GGEAFYRYFMGLTEWE	14.8	8.4	12.9	0.7	1.5	
NNRPα-1-B4-IR	LSSGFYRYFTGLSDGQ	19.1	6.3	9.2	0.7	1.5	
NNRPα-4-D9-IR	DPGAFYRYFAQLMDTWN	7.6	16.9	25.7	0.7	1.5	
NNRPβ-4-F2-IR	KHEQFYRYFRNLLGAMS	21.6	20.9	30.8	0.7	1.5	
NNRPβ-4-H12-IR	RDCAFYRYFEDLLIAVD	5.2	13.8	20.0	0.7	1.5	
NNRPα-4-E7-IR	RCNRFYRYFEYLLRDYG	9.4	21.9	29.7	0.7	1.4	
NNRPα-1-B5-IR	ELGDFYRYFQLLADWH	14.1	5.4	7.1	0.8	1.3	
NNRPα-4-C4-IR	AQDAFYSYFSVLLGEHL	17.6	17.6	22.3	0.8	1.3	
NNRPα-4-C7-IR	IGVNFYRYFEKLLDEF	4.5	11.2	14.9	0.8	1.3	
NNRPα-4-D3-IR	TDSQFYSYFESLLETFC	16.4	13.5	17.9	0.8	1.3	

FIGURE 2P



Clone Design	Sequence	Ratios over Background				Comparisons	
	XXXXXXXXFYRYFXLLXXXXXXXX	E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
NNRPβ-4-G10-IR	SSREFSYFSGLTTVAL	8.8	8.7	11.7	0.7	1.3	
NNRPβ-4-H2-IR	TGRGFYRYFEGLLDWM	4.9	19.9	25.3	0.8	1.3	
NNRPα-4-C1-IR	SGSWFYRYFEEELLQSG	15.5	18.0	21.1	0.9	1.2	
NNRPα-4-C5-IR	GRGIFYQYFLDLLQTEA	18.0	23.3	26.9	0.9	1.2	
NNRPα-4-C6-IR	GQNGFYRYFDTLADWV	7.8	13.6	15.7	0.9	1.2	
NNRPα-4-C12-IR	FAGSFYRYFEQLLSEQ	12.3	16.7	19.9	0.8	1.2	
NNRPα-4-D7-IR	DPNAFYRYFEGLLWREH	10.2	23.7	27.9	0.8	1.2	
NNRPα-4-D11-IR	?GLNFYRYFVGLTDTL	5.4	19.3	22.3	0.9	1.2	
NNRPβ-4-F1-IR	RHINFYGYFDDLATWH	21.7	23.0	28.6	0.8	1.2	
NNRPβ-4-F9-IR	FHRGFYRYFINLLSGDA	10.1	18.4	22.5	0.8	1.2	
NNRPβ-4-F12-IR	MGSSFYRYFETLLGQGL	4.5	13.5	16.6	0.8	1.2	
NNRPγ-4-A3-IR	GSLDFYSYFMERLGLGP	16.4	22.3	26.8	0.8	1.2	
NNRPα-1-A7-IR	STVSFYRYFYALLQSPC	16.9	1.2	1.3	0.9	1.1	
NNRPα-4-C11-IR	LGIFYRYRFEDLLNHQS	7.8	19.7	21.2	0.9	1.1	
NNRPα-4-D8-IR	DHRGFYRYFLYQLAGNV	6.9	17.6	20.1	0.9	1.1	
NNRPα-4-D10-IR	EYSGFYGYFMHLLGSLG	6.4	17.2	19.5	0.9	1.1	
NNRPα-4-E5-IR	TSNWFYQYFTDLLAGED	13.2	26.1	27.6	0.9	1.1	
NNRPα-4-E8-IR	SSGCFYRYFSQLLTEMN	8.7	22.9	24.2	0.9	1.1	
NNRPα-4-E10-IR	VHGEFYRYFESLLRETF	3.5	12.4	13.2	0.9	1.1	
NNRPβ-4-F8-IR	SDEGFYRYFAQLLYGVT	8.1	22.9	25.2	0.9	1.1	
NNRPβ-4-F10-IR	ETGIFYGYFQALATYH	5.3	17.9	19.1	0.9	1.1	
NNRPβ-4-G8-IR	GDRGFYRYFEWLLNDFG	10.6	27.2	28.9	0.9	1.1	
NNRPβ-4-H3-IR	FGGAFYRYFEALLGEMG	3.9	24.2	25.7	0.9	1.1	
NNRPβ-4-H9-IR	DGGAFYRYFEALLGELD	4.1	26.5	29.3	0.9	1.1	
NNRPβ-4-H10-IR	WHSDFYRYFLSLQEDG	3.4	22.3	24.6	0.9	1.1	
NNRPγ-4-A6-IR	EEEGFYGYFYRLLGVER	14.9	25.8	27.6	0.9	1.1	
NNRPγ-4-A8-IR	MDAGFYGYFSDLANWG	9.8	22.8	24.7	0.9	1.1	

FIGURE 2P (Con't)



Clone Design	Sequence	E-Tag	ICFR	IR	ICFR/IR	IR/ICFR
NNRPy-4-A10-IR	XXXXXXXXFYRYFXLLXXXXXXXX	--	--	--	--	--
NNRPy-4-B6-IR	SGFAFYQYFQELLAGHD	7.6	20.3	22.0	0.9	1.1
NNRPy-4-B9-IR	GDGCFYGYFASLLSGEG	12.2	22.3	24.2	0.9	1.1
NNRPa-4-C8-IR	EANGFYRYFYDLLQDFG	6.7	22.9	25.9	0.9	1.1
NNRPa-4-C9-IR	AVNGFYRYFNRLLSEVE	8.5	16.3	16.0	1.0	1.0
NNRPa-4-C10-IR	QQDGFYRYFLDLDEVA	5.6	20.7	19.9	1.0	1.0
NNRPa-4-E11-IR	ISQGFYGYFSRLLQDTE	6.7	16.5	17.2	1.0	1.0
NNRPl-4-F11-IR	YSTGFYRYFLDLLDGMF	6.0	20.3	20.9	1.0	1.0
NNRPl-4-G2-IR	PNGDFYRYFLDLLGSVG	7.7	21.8	21.9	1.0	1.0
NNRPl-4-G9-IR	RHQAFYSYFRDLPRECP	19.1	24.7	25.6	1.0	1.0
NNRPl-4-H7-IR	ETEGFYRYFEELLAQVA	7.8	27.3	26.4	1.0	1.0
NNRPl-4-H8-IR	AGDRFYDYFDRLLDYD	2.6	26.6	27.9	1.0	1.0
NNRPY-4-B1-IR	GGSGFYRYFWGLLAQGE	3.6	23.0	24.1	1.0	1.0
NNRPY-4-B10-IR	LLNRLYRYFAGAECWFG	17.6	24.5	23.4	1.0	1.0
NNRPa-1-B3-IR	DGSGFYRYFEMLLGSGL	5.5	18.3	19.0	1.0	1.0
NNRPa-2-C2-IR	RDMAFYRYFSHLLSEFQ	16.4	13.4	12.7	1.1	0.9
NNRPa-2-C3-IR	GNAGFYRISRILMQGTE	22.5	24.4	21.3	1.1	0.9
NNRPa-2-D10-IR	GNAGFYRYFADLMAGYE	19.6	21.7	19.7	1.1	0.9
NNRPa-3-E11-IR	YQAAFYRYFATLLSTTD	17.8	6.3	5.4	1.2	0.9
NNRPa-3-F5-IR	GGLGFYRYFQLLLGSSG	12.9	10.8	9.6	1.1	0.9
NNRPa-3-F8-IR	DGSGFYGYFDVLRQFE	25.1	18.3	17.0	1.1	0.9
NNRPa-3-F10-IR	VGSGFYRYFDQLLGMYG	22.2	15.7	13.9	1.1	0.9
NNRPa-3-G7-IR	YGTDFYLYFDQLLLQYG	20.5	14.6	13.1	1.1	0.9
NNRPa-4-C2-IR	FNSSFYLYFRDLLNTVG	21.0	18.3	15.6	1.2	0.9
NNRPa-4-D12-IR	RAAGFYRYFEDLLGARG	25.5	25.1	23.3	1.1	0.9
NNRPl-4-G3-IR	TGAGFYRYFIDLGETG	14.7	19.7	18.5	1.1	0.9
NNRPl-4-G4-IR	RDLEFYGYFQELRLNF	14.6	27.8	25.7	1.1	0.9
NNRPY-4-A5-IR	GMGPFYRYFIDLLRESD	20.0	28.6	24.9	1.1	0.9
NNRPY-4-A5-IR	HGDGFYQYFMEVLRLLQ	17.0	29.0	27.3	1.1	0.9

FIGURE 2P (Con't)





Clone Design	Sequence XXXXXXXXXXFYRYFXLLXXXXXXXXXX	E-Tag --	IGFR --	IR --	IGFR/IR --	IR/IGFR --
NNRPy-4-A12-IR	AFYRYFRDLJFSGF	4.9	16.3	14.9	1.1	0.9
NNRPy-4-B8-IR	DDRGFYRYFESLLGSS	6.1	21.3	19.9	1.1	0.9
NNRPy-1-A5-IR	LSTSFYQYLACLLRGDR	2.3	1.4	1.1	1.2	0.8
NNRPy-1-B7-IR	GSSGFYRYFNMMLSQT	19.2	15.7	12.4	1.3	0.8
NNRPy-2-C7-IR	GDRGFYRYFEGCLASVC	19.6	20.0	16.5	1.2	0.8
NNRPy-2-C11-IR	NSAFYRYFEQLLREVEV	20.1	20.0	16.3	1.2	0.8
NNRPy-2-C12-IR	LSDFYRYFEQLMGARS	14.3	10.1	8.5	1.2	0.8
NNRPy-2-D12-IR	RSTLFYRYFQNLLEEVG	11.5	11.4	9.3	1.2	0.8
NNRPy-3-G2-IR	TRGGFYRYFEDLLQVYS	20.8	20.7	16.1	1.3	0.8
NNRPy-3-G8-IR	GVS GFYRYFQSLDPSYG	14.7	11.0	9.2	1.2	0.8
NNRPy-3-G10-IR	QNDAFYSYFNSLLQAYT	18.8	16.5	13.9	1.2	0.8
NNRPy-3-G11-IR	RQQDFYRYFRQLLEEV	12.0	10.3	8.5	1.2	0.8
NNRPy-3-G12-IR	EGSGFYRYFEKLLQSP	11.7	11.8	9.3	1.3	0.8
NNRPy-4-B2-IR	RHKA FYRYFEELLQKNV	22.8	30.3	25.3	1.2	0.8
NNRPy-1-B8-IR	GRMTRLIVRSTVISRELLHYSL	16.1	10.1	6.9	1.5	0.7
NNRPy-2-C5-IR	QALS FYRYFERLLDEV3	18.1	19.2	13.7	1.4	0.7
NNRPy-2-C9-IR	SKSAFYRYFDELLGNSG	22.9	21.7	16.1	1.3	0.7
NNRPy-2-D2-IR	LGGA FYRYFAQLNSHV	26.1	26.2	17.6	1.5	0.7
NNRPy-2-D5-IR	LNSGFYGYFVQLLSGHQ	21.7	21.1	15.4	1.4	0.7
NNRPy-2-D11-IR	SQSSFYRYFESLLEDPN	12.3	10.8	7.8	1.4	0.7
NNRPy-3-E2-IR	ADGGFYGYFAALLGSVS	24.4	25.5	18.3	1.4	0.7
NNRPy-3-E4-IR	QNGSFYRYFIALLDPSG	23.0	22.3	14.7	1.5	0.7
NNRPy-3-F4-IR	WDTGFYRYFIELLEDRD	24.9	25.1	17.6	1.4	0.7
NNRPy-3-G4-IR	HPRDFYRYFERLLNQVD	20.9	20.4	14.1	1.5	0.7
NNRPy-3-H4-IR	DGGA FYRYFMDLLGAHE	17.7	17.6	11.6	1.5	0.7
NNRPy-4-E12-IR	AGRGFYRYFEHLLAGRE	4.3	15.4	10.8	1.4	0.7
NNRPy-4-G11-IR	SSRGFYRYFRELLADSW	6.6	18.4	13.1	1.4	0.7
NNRPy-4-H6-IR	KYSGFYRYFNALLGRRE	2.2	16.1	11.7	1.4	0.7

FIGURE 2P (Con't)



502879_1

Clone Design	Sequence	E-Tag	ICFR	IR	ICFR/IR	IR/ICFR
NNRPβ-4-H11-IR	XXXXXXXXFYRYFXLXXXXXXXX	--	--	--	--	--
NNRPα-1-B1-IR	DYTA FYGYFNNLRTSG	2.3	12.4	9.0	1.4	0.7
NNRPα-2-D7-IR	FQSSFYGYFESLMSYK	18.8	18.7	11.5	1.6	0.6
NNRPα-3-E1-IR	DTNAFYRYFEGLLMSEH	21.0	21.8	13.2	1.6	0.6
NNRPα-3-H3-IR	GGSSFYRYFEQLLAQME	20.2	19.8	12.2	1.6	0.6
NNRPα-3-H5-IR	SQGGFYRYFEKLDEVT	20.0	20.5	12.9	1.6	0.6
NNRPα-1-A3-IR	RSGLFYRYFEELLQAI	20.0	24.5	15.5	1.6	0.6
NNRPα-3-F9-IR	QGGGFYHYFLSLLEVG	19.8	19.1	12.2	1.6	0.6
NNRPα-3-G6-IR	WRGA FYRYFQTLLSDEG	19.9	18.0	11.1	1.6	0.6
NNRPα-3-H9-IR	AAGFYGYFYSLLGDQT	24.4	14.9	7.9	1.9	0.5
NNRPα-1-A8-IR	RNSGFYRYFQHLVSEWE	23.1	19.0	9.6	2.0	0.5
NNRPα-3-F6-IR	QHRLFYSYFAELLGRDT	21.1	18.8	9.6	1.9	0.5
NNRPα-3-H2-IR	QIDEFYRYFADQLRGFA	22.4	17.7	9.0	2.0	0.5
NNRPα-2-D6-IR	LGGGFYRYFNLVMSG	18.3	13.1	6.9	1.9	0.5
NNRPα-1-A9-IR	GDRA FYRYFQRLGEGWG	16.9	13.8	5.7	2.4	0.4
NNRPα-3-H1-IR	CEDAFYRYFVNLLQGC	16.5	15.2	5.6	2.7	0.4
NNRPα-2-D6-IR	NYSQFYRYFEMLEGDV	19.4	18.5	6.8	2.5	0.4
NNRPα-3-F6-IR	VGDA FYRYFQGLLRDQ	22.8	19.5	7.9	2.2	0.4
NNRPα-3-H2-IR	MHGSFYRYFQDLLQAP	19.9	18.9	8.5	2.2	0.4
NNRPα-1-B6-IR	DVGDFYRYFGLLTSDR	14.1	11.5	3.9	3.0	0.3
NNRPα-2-C6-IR	NSA FYGYFSQLLAQIR	18.4	19.2	4.1	4.7	0.2
NNRPα-4-A1-IR	IIGGFYSYFNSVRLGT	9.7	10.9	1.8	6.0	0.2
NNRPα-4-A7-IR	RDPFYSYFVNLLGASA	2.5	6.3	1.3	4.9	0.2
NNRPα-4-A9-IR	EGSGFYGYFFSLGLQG	3.0	10.0	1.4	7.1	0.1
NNRPα-4-B11-IR	LKDG FYDYFWORLHGS	4.1	18.7	1.2	15.5	0.1

FIGURE 2P (Cont.)



Clone
Design
R20-4-F9-IGFR
R20-4-H4-IGFR
R20-4-F9-IGFR
R20-4-D6-IGFR
R20-4-G2-IGFR

Sequence
XXXXXXXXXXXXXXXXXXXX
PLAELWAYFEHSEQGRSSAH
PVLSGLLRYFAGGPLGQPS
GGYLDLWMHYFRDGOALQPM
VDOROGWMLLALENYFRSTV
DVPAGGLLRQMWVYFRPSDP

Ratios over Background				Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
--	--	--	--	--	--
33.1	19.3	1.0	19.3	0.1	
24.1	5.6	3.2	1.8	0.6	
2.5	2.4	1.4	1.7	0.6	
6.1	2.9	1.9	1.5	0.7	
6.3	2.2	2.0	1.1	0.9	

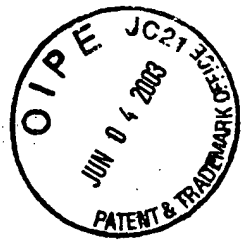
Figure 3A

Clone
Design
20C-3-F3-IGFR

Sequence
XXXXXXXXXXXXXXXXXXXX
RRVACTQADGDLCESDPLKALLSYF

Ratios over Background				Comparisons	
F-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
35.5	32.8	17.9	1.8	0.5	

Figure 3B



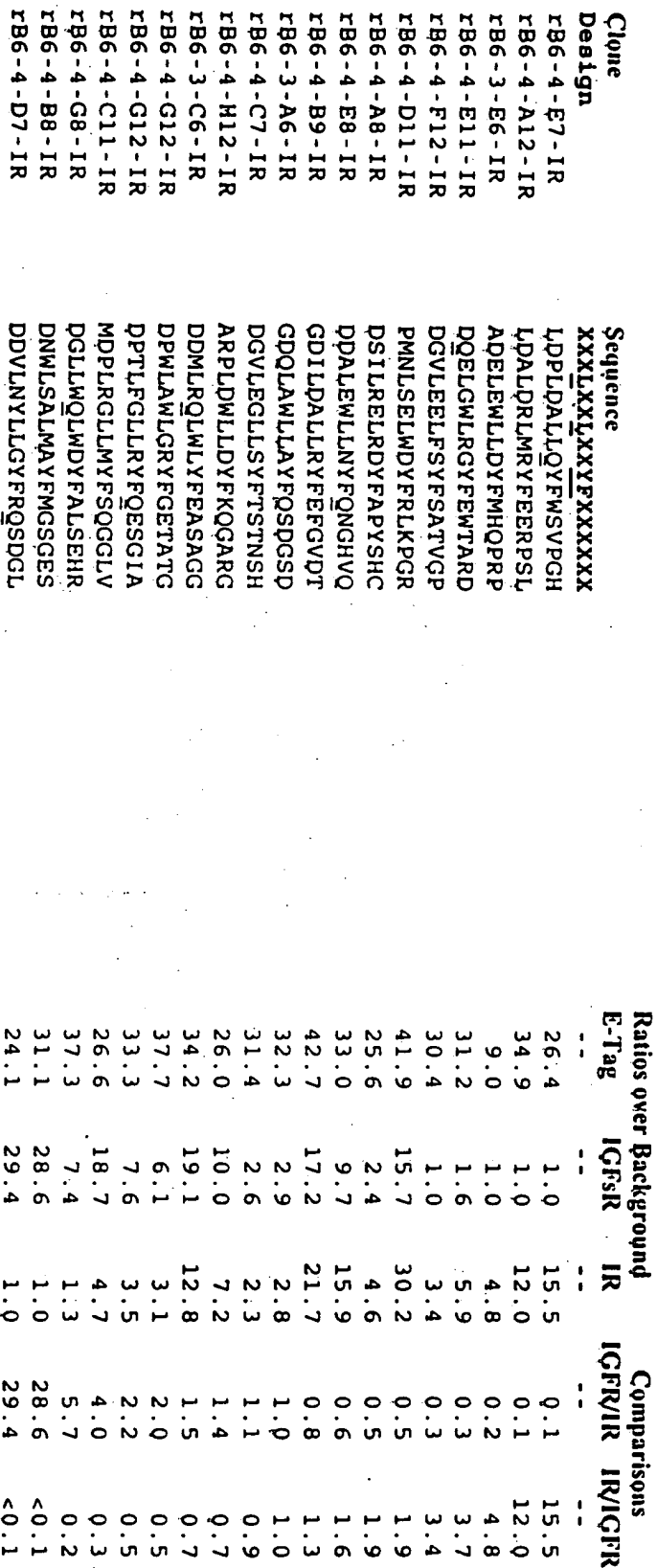


Figure 3C

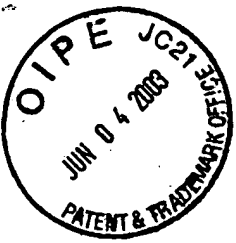
Clone	Sequence	Ratios over Background				Comparisons	
Design	XXXXLXXLXXYFXXXXXX	E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	--
RB6-4-B10-IGFR	RPVLGWLFDYFVASDPM	33.1	26.9	1.0	26.9	<0.1	
RB6-3-E6-IGFR	RWPLSALMDYFRRSQGV	37.6	26.6	1.0	26.6	<0.1	
RB6-4-B9-IGFR	DGVLASLWRYFVSGGTL	39.2	26.3	1.0	26.3	<0.1	
RB6-3-F5-IGFR	DRQLGWLMDYFHLTDLR	33.2	15.6	1.0	15.6	0.1	
RB6-3-B6-IGFR	DGILGLMAYFVES?RV	37.4	13.3	1.0	13.3	0.1	
RB6-3-D4-IGFR	QDLLGRMLYFAETDTV	31.2	20.7	2.0	10.4	0.1	
RB6-4-D10-IGFR	SGVLADLFRYFQRHPMP	31.7	10.1	1.0	10.1	0.1	
RB6-3-D6-IGFR	DPPLGGLWTYFSRSDPG	33.9	9.9	1.0	9.9	0.1	
RB6-4-F9-IGFR	DSVLSLYSYFASGDLA	34.3	28.3	3.0	9.4	0.1	
RB6-3-E1-IGFR	DGVLAALEAYFRHGPRD	30.5	9.3	1.0	9.3	0.1	
RB6-3-B2-IGFR	DEILGALYSYFSLSGA	22.2	8.8	1.0	8.8	0.1	
RB6-3-D7-IGFR	QPVLGALQRYFASGEPM	31.2	7.6	1.0	7.6	0.1	
RB6-4-C11-IGFR	DSVLQYLLNHFGADSKO	33.7	7.6	1.0	7.6	0.1	
RB6-4-F12-IGFR	NEVLEGLFSYFVY?ANG	38.1	7.3	1.0	7.3	0.1	
RB6-4-F7-IGFR	SGILGQLLRYFKGAGGG	38.6	7.3	1.0	7.3	0.1	
RB6-3-G6-IGFR	PELLDRLMQYFQVGGDL	34.0	7.1	1.0	7.1	0.1	
RB6-4-E8-IGFR	PGILLDLWRYFASAPDQ	37.6	6.9	1.0	6.9	0.1	
RB6-4-G10-IGFR	DSVLLDLYEYFSSGSSG	34.9	14.5	2.2	6.6	0.2	
RB6-4-B12-IGFR	DGMLSRIMEYFAGTNVP	36.3	28.9	4.5	6.4	0.2	
RB6-3-B5-IGFR	DVILGGLMDYFASGGCH	17.2	6.1	1.0	6.1	0.2	
RB6-3-C5-IGFR	GGVLAALERFYFVSAGD	38.7	15.8	2.9	5.4	0.2	
RB6-4-B8-IGFR	DEVLGRLMAYFAQESLG	31.9	22.0	4.1	5.4	0.2	
RB6-3-H2-IGFR	DGILQSLMDYFARSPVG	31.8	22.4	4.2	5.3	0.2	
RB6-3-E5-IGFR	VDILSELMDYFRGEEG	37.0	20.5	4.0	5.1	0.2	
RB6-3-B3-IGFR	DKVLRLLGEYFATHSKG	31.7	4.8	1.0	4.8	0.2	
RB6-4-G7-IGFR	QGPLAWLRDYFASGTRS	37.4	10.0	2.1	4.8	0.2	
RB6-3-A3-IGFR	QDVLRSLLSYFMGNGDV	27.2	4.7	1.0	4.7	0.2	
RB6-4-E9-IGFR	DGVLSKLWEYFKIQGND	37.3	20.1	4.8	4.2	0.2	

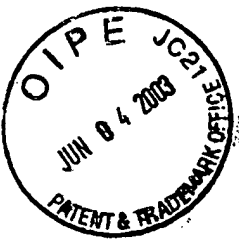
Figure 3D



Clone	Sequence	Ratios over Background				Comparisons	
Design		E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
Clone	Sequence	--	--	--	--	--	--
RB6-3-F1-IGFR	XXXLXXLXXYFXXXXXX	26.5	5.8	1.4	4.1	0.2	
RB6-4-B7-IGFR	NTILGDLWRYFAGSGM	31.1	11.4	2.9	3.9	0.3	
RB6-4-C10-IGFR	?DVLKKL?VYFELSGA	32.2	3.7	1.0	3.7	0.3	
RB6-3-A1-IGFR	DRLLSGLWAYFAGNGGS	21.1	3.5	1.0	3.5	0.3	
RB6-3-F6-IGFR	DLILQSLLDYFQGRPVG	25.1	3.5	1.0	3.5	0.3	
RB6-3-H5-IGFR	LALLPMLWDYFVATDPQ	35.5	18.1	5.6	3.2	0.3	
RB6-4-D8-IGFR	DSLRLRLDYFARTHIA	36.2	22.5	7.5	3.0	0.3	
RB6-4-A8-IGFR	DGVLGQLWQYFAQYPGS	41.1	30.6	10.6	2.9	0.3	
RB6-4-H8-IGFR	?PPLDALMEYFTGTARD	38.7	33.0	11.5	2.9	0.3	
RB6-3-E2-IGFR	DNVLEGLMSYFALMSQL	20.9	2.2	1.0	2.2	0.5	
RB6-3-C2-IGFR	SAVLEYLLAYFARTGAA	31.0	2.1	1.0	2.1	0.5	
RB6-4-G8-IGFR	DRALGPLWRYFMVNNCG	38.7	5.5	2.6	2.1	0.5	
RB6-3-G5-IGFR	WRILDRLLAYFKESQGD	32.8	2.0	1.0	2.0	0.5	
RB6-4-C9-IGFR	DDVLVTLFQYFRASSTGV	37.6	30.2	15.1	2.0	0.5	
RB6-4-D11-IGFR	FDVLTWLGRYF*MNTGK	36.6	5.5	3.0	1.8	0.5	
RB6-4-B11-IGFR	RDVLDTGLREYFRASVCG	25.2	4.2	2.4	1.8	0.6	
RB6-4-E11-IGFR	IKTLNDLLAYFRGDLQV	38.1	29.8	22.2	1.3	0.7	
RB6-3-G3-IGFR	DEALMLMRYFRGSPSP	31.6	8.7	7.2	1.2	0.8	
RB6-4-H12-IGFR	ESPLDALRAYFSGRRNW	40.1	2.8	2.5	1.1	0.9	
RB6-4-G12-IGFR	IQSL*DLLQYFVSSPSV	36.7	32.5	31.4	1.0	1.0	
RB6-3-C4-IGFR	GGILD?LQDYFRSTDVG	37.1	6.2	13.5	0.5	2.2	

Figure 3D (Con't)





Clone
Design
R2013-4-F8-IR

Sequence
XXXXXXXXXXXXXXXXXXXX
HLCVLEELLFWGASLFGYCSCG

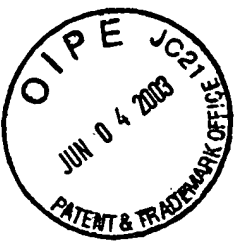
Ratios over Background			Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR
--	--	--	--	--
39.1	1.8	27.7	0.1	15.4

Figure 4A



Clone	Design	Sequence	Ratios over Background		Comparisons	
			E-Tag	ICFR	IR	ICFR/IR IR/ICFR
	F815-4-H9-IR	HLCVLEELFMGASLFGXCSCG	--	--	--	--
	F815-3-B1-IR	PLCVLEELFMSTPLFGQCSY	34.9	0.9	37.6	<0.1 40.8
	F815-3-B1-IR	HLCVLEELFMGASLFAQCVC	31.7	0.9	35.8	<0.1 39.3
	F815-3-Q1-IR	PLCVLEELFMGASRFGQCSG	30.4	0.9	33.5	<0.1 38.9
	F815-3-Q4-IR	HLCVLEELFMGASLFGQCAQ	31.5	0.9	33.6	<0.1 38.8
	F815-3-C5-IR	HLCVLEELFMGASLFGQCSG	31.1	0.8	31.2	<0.1 38.5
	F815-4-H3-IR	NLCVLEELFMGASLFRQCSG	33.7	1.0	37.2	<0.1 38.4
	F815-3-A5-IR	PLCVLEELFMGASLFGQCSG	37.4	1.1	40.9	<0.1 38.3
	F815-3-D7-IR	QLCVLEELFMGASEFGQCSG	33.6	0.9	34.3	<0.1 38.3
	F815-3-A1-IR	HLCVLEELFMGASLFGQCSG	29.8	0.9	34.8	<0.1 38.0
	F815-3-A3-IR	PLCVLEELFMGESLFGQCSG	31.1	0.9	32.7	<0.1 38.0
	F815-3-A3-IR	HLCVLEELFMGASRFGQCSG	32.8	1.0	39.1	<0.1 37.9
	F815-3-B3-IR	KLCVLEELFMGASLFGQCSG	33.7	1.0	37.5	<0.1 37.5
	F815-3-A4-IR	YLCVLEELFMGASLFGQCSG	32.5	1.0	36.9	<0.1 37.5
	F815-3-D2-IR	HLCVLEELFMGASLFAQCSCG	31.9	0.9	34.1	<0.1 37.4
	F815-3-C4-IR	QLCVLEELFMGESLFGQCSG	31.6	0.8	31.8	<0.1 37.4
	F815-3-B4-IR	HLCVLEELFMGASLFGQCSG	33.8	1.0	36.7	<0.1 37.3
	F815-3-C1-IR	SLCVLEELFMGASLFGQCSG	29.0	0.9	35.0	<0.1 37.3
	F815-4-G9-IR	HLCVLEELFMGASLFGQCSG	36.5	1.0	38.9	<0.1 37.1
	F815-4-G6-IR	QLCVLEELFMGASLFGQCSG	34.9	1.0	36.4	<0.1 37.0
	F815-3-A8-IR	PLCVLEELFMGASLFGQCSG	34.7	1.1	39.3	<0.1 36.9
	F815-4-G5-IR	PLCVLEELFMGASLFGQCSG	26.5	1.0	35.1	<0.1 36.8
	F815-3-B5-IR	HLCVLEELFMGASLFGQCSG	33.2	0.9	34.1	<0.1 36.8
	F815-4-F4-IR	PLCVLEELFMGASLFGQCSG	28.6	0.8	30.0	<0.1 36.7
	F815-3-A2-IR	QLCVLEELFMGASLFGQCSG	32.5	1.0	36.6	<0.1 36.6
	F815-3-B6-IR	HLCVLEELFMGASLFGQCSR	31.6	0.9	32.9	<0.1 36.5
	F815-4-H7-IR	PLCVLEELFMGASLFGQCSG	33.7	1.0	37.6	<0.1 36.4
	F815-4-H8-IR	QLCVLEELFMGASLFGQCSG	35.8	1.0	37.0	<0.1 36.4
	F815-4-G7-IR	NLCVLEELFMGASLFGQCSG	33.7	1.0	35.8	<0.1 36.3

Figure 4B



Clone	Design	Sequence	Ratios over Background		Comparisons	
			E-Tag	IGFSR	IR	IGF/IR
		<u>HLCVLEELFMGASLFGYCSG</u>	--	--	--	--
F815-3-A6-IR		QLCVLEELFMGSSLFGQCSG	34.6	1.1	39.0	<0.1
F815-3-D3-IR		PLCVLEELFMGKSLFGQCSG	33.8	1.0	36.2	<0.1
F815-3-B12-IR		PLCVLEELFMGSSLFGQCSG	33.2	1.0	35.7	<0.1
F815-4-G10-IR		YLCVLEELFMGASLFRQCSG	35.4	1.0	37.2	<0.1
F815-4-E3-IR		HLCVLEELFMGSSLFGQCSG	32.4	1.0	35.0	<0.1
F815-4-E6-IR		PLCVLEELFMGASLFGQCSG	33.2	1.0	34.5	<0.1
F815-4-F1-IR		HLCVLEELFMGASLFGQCSG	29.4	0.9	32.5	<0.1
F815-4-G8-IR		PLCAIEELFMGASLFGQCSG	36.8	1.1	38.2	<0.1
F815-4-H12-IR		HLCVLEELFMGASLFGQCSG	30.5	0.9	31.9	<0.1
F815-4-G3-IR		PLCVLEELFMGASLFGQCSG	31.4	1.0	35.7	<0.1
F815-3-C2-IR		PLCVLEELFMGASLFGQCSG	32.3	1.0	36.1	<0.1
F815-4-E10-IR		QLCVLEELFMGASLFGQCSG	35.4	1.0	36.5	<0.1
F815-3-A12-IR		HLCVLEELFMGASLFGQCSG	32.1	1.0	36.3	<0.1
F815-3-B8-IR		HLCVLEELFMGASLFGQCSG	33.6	1.0	35.8	<0.1
F815-3-B2-IR		HLCVLEELFMGASLFGQCSG	31.0	1.0	35.3	<0.1
F815-3-C3-IR		PLCVLEELFMGASLFGQCSG	30.1	1.0	35.3	<0.1
F815-3-A7-IR		HLCVLEELFMGASLFGQCSG	33.1	1.0	35.8	<0.1
F815-4-F9-IR		RLCVLEELFMGASLFGQCSG	33.4	1.0	35.7	<0.1
F815-3-B7-IR		QLCVLEELFMGASLFGQCSG	32.0	1.0	33.5	<0.1
F815-4-E4-IR		HLCVLEELFMGASLFGQCSG	28.0	1.0	33.4	<0.1
F815-4-E12-IR		YLCVLEELFMGASLFGQCSG	28.0	0.9	30.2	<0.1
F815-4-F8-IR		HLCVLEELFMGASLFGQCSG	33.8	1.0	35.2	<0.1
F815-3-C7-IR		HLCVLEELFMGASLFGQCSG	33.9	1.0	34.7	<0.1
F815-4-F10-IR		PLCVLEELFMGASLFGQCSG	32.7	1.0	34.2	<0.1
F815-3-D11-IR		HLCVLEELFMGASLFGQCSG	35.4	1.1	37.3	<0.1
F815-4-E7-IR		HLCDLEELFMGASLFGQCSG	30.3	0.9	32.2	<0.1
F815-3-A10-IR		QLCVLEELFMGASLFGQCSG	34.0	1.1	36.4	<0.1
F815-3-B11-IR		ALCVLEELFMGASLFGQCSG	33.7	1.1	36.3	<0.1

Figure 4B (Con't)



Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	ICFSR	IR	ICFR/IR IR/ICFR
F815-4-F11-IR	<u>HL</u> CVLEELFWGASLFGYCSG	--	--	--	--
F815-3-A9-IR	RLCVLEERFWGA L ALFGQCSG	31.8	1.0	33.7	<0.1 34.2
F815-4-G11-IR	PLCVLEELFWGASLFGQCSG	31.9	1.0	35.5	<0.1 34.1
F815-3-D8-IR	SLCVLEELFWGASLFGQCSG	32.3	1.0	34.4	<0.1 33.9
F815-4-G4-IR	HLCLLEEQFWGASLFGYCFE	32.3	1.0	33.3	<0.1 33.7
F815-3-C8-IR	HLCVLEEQFWGASLFGQCSG	23.8	1.0	32.2	<0.1 33.7
F815-4-G12-IR	PLCLLEELMWGASLFGQCSG	33.9	1.0	35.1	<0.1 33.6
F815-3-D12-IR	YLCVLEERFWGASLFGQCSG	31.7	1.0	33.5	<0.1 33.5
F815-4-F7-IR	HLCVLEEQFWGASLFGSCSG	33.3	1.0	34.8	<0.1 33.4
F815-4-F2-IR	QLCVLEEQFWGASLFGQCSG	33.3	1.0	34.3	<0.1 33.4
F815-3-B9-IR	HLCVLEELF*GESLFGYCSG	26.1	1.0	33.8	<0.1 33.3
F815-4-H2-IR	HLCVLEELFWGASLFGQCSG	33.6	1.1	35.7	<0.1 33.2
F815-4-E11-IR	PLCVLEELFWGASHFGQCSG	36.1	1.2	38.4	<0.1 33.0
F815-4-G1-IR	HLCVLEELMWGASLFGQCSG	33.2	1.1	35.4	<0.1 32.8
F815-3-A11-IR	QLCVLEELMWGASLFGQCSG	27.9	1.0	31.5	<0.1 32.7
F815-4-F6-IR	HLGLEELFWGASLFGQCSG	37.7	1.2	40.1	<0.1 32.6
F815-3-D9-IR	RLCVLEELVWGASLFGQCSG	32.3	1.1	34.6	<0.1 32.5
F815-4-G2-IR	RLCVLEELFWGASLFGQCSG	31.4	1.0	32.5	<0.1 31.9
F815-3-C9-IR	HLCLLEELFWGATLFDQCSG	33.4	1.1	35.7	<0.1 31.4
F815-4-H10-IR	HLCFLEELFWGASLFGQCSG	30.2	1.1	34.3	<0.1 31.0
F815-4-F3-IR	HLCLVEELFWA P PLFGQCSG	29.7	1.0	31.4	<0.1 29.4
F815-4-F5-IR	HLCVLEELMWGASLFAQCSA	31.9	0.9	27.6	<0.1 28.9
F815-4-H1-IR	NLCVLEELFWGASQFRYCPG	19.4	1.0	28.0	<0.1 26.8
F815-4-E5-IR	RLCVLEELFWGASLFGQCSG	12.3	0.9	24.8	<0.1 16.5
F815-4-H5-IR	PLCVLEELFWGASLFGQCPG	6.9	1.0	15.8	0.1 14.0
F815-3-C10-IR	NLCVLEELFWGASLFGQCSG	3.5	1.0	13.6	0.1 13.5
	QLCVLG#RFGGSLGYS	5.5	1.0	13.1	0.1 4.5
	QLCVLG#RFGGSLGYS	3.5	1.1	5.2	0.2

Figure 4B (Con't)



Clone	Sequence
Parental/Design	<u>HLCVLEELFMGASLFGYC</u> SG
F815-4-F11-IGFR	PLCF L Q E LFGGASLGGYC
F815-4-E12-IGFR	FMCG L Q E LVGGALLGHC
F815-4-H10-IGFR	PLCF L Q E LFGGSLSGYC
F815-4-B7-IGFR	FLCGLEELAMGVSRSYC
F815-3-B5-IGFR	PLCF L AE L FSGSALGDC
F815-4-D12-IGFR	PLCV L Q E LFGGSLGGYC
F815-4-C11-IGFR	QLCV L E L LFMGAC L FGYC
F815-4-C7-IGFR	FLCG L Q E LSGVASLFG Q C
F815-4-E7-IGFR	RVCV L EQ L VWGASLFGA*SG
F815-4-G7-IGFR	FYCGLEELSMGALFGYC
F815-4-A10-IGFR	FLCGLEEL S Q G AVLFGHC
F815-3-B3-IGFR	HLCV L VGLFWDASLFG Q C
F815-3-G1-IGFR	QRCIRALFWCATLLGCG
F815-4-G12-IGFR	HQ C IPDGMSQGAALRGNC
F815-3-H1-IGFR	HLCVLEDELWGVSLFGYC

Ratios over Background					Comparisons	
E-Tag	IGFR	IR	IGFR/IR	IR/IGFR		
39.1	1.8	27.7	0.1	15.4		
33.4	12.3	1.0	12.3	0.1		
33.7	15.1	1.7	8.9	0.1		
30.1	8.5	1.0	8.5	0.1		
35.2	23.9	4.8	5.0	0.2		
33.9	4.8	1.0	4.8	0.2		
33.6	7.0	1.8	3.9	0.3		
13.9	4.6	1.8	2.6	0.4		
16.8	2.0	1.0	2.0	0.5		
26.9	3.8	1.9	2.0	0.5		
30.4	9.0	5.0	1.8	0.6		
30.8	3.7	2.2	1.7	0.6		
7.6	1.0	2.0	0.5	2.0		
20.5	1.0	2.0	0.5	2.0		
7.6	1.0	2.5	0.4	2.5		
18.4	1.0	6.8	0.1	6.8		

Figure 4C

Clone	Sequence	Ratios over Background				Comparisons	
Parental/Design		E-Tag	IGF ^R	IR	IGF ^R /IR	IR/IGF ^R	
F820-4-B5-IR	<u>HLCLLEELFWGASLFGYCSG</u>	39.1	1.8	27.7	0.1	15.4	
F820-4-B5-IR	<u>HLCLLEELFWGASLFGYCSG</u>	28.1	0.9	17.9	<0.1	21.1	
F820-4-A2-IR	TCAFWKNGSGVRRCSVTAVV	34.0	1.6	22.7	0.1	13.9	
F820-4-E2-IR	PLCGLKN.SGVRICSSPALV	21.3	0.7	9.0	0.1	13.4	
F820-4-D10-IR	PLCLQEEELFWGASLFGYCSG	34.1	1.0	12.1	0.1	12.1	
F820-4-H7-IR	PLCDLEELFWGASLFGDCPQ	14.2	0.6	6.5	0.1	11.6	
F820-4-G6-IR	DLCLLEELFWDGSIFASCSCG	14.0	0.5	6.1	0.1	11.5	
F820-4-C2-IR	PLCVLEELQMWGTALFGSCTG	38.1	1.2	11.8	0.1	9.9	
F820-4-B4-IR	PLCLVEELLMGASLFSQCTG	15.1	0.7	6.4	0.1	8.7	
F820-4-C7-IR	PLCDLEELYMGALLFGSCSCG	46.3	2.7	22.2	0.1	8.2	
F820-4-F10-IR	GLCFLEELQFWGTSLFRDCPG	14.5	0.6	4.7	0.1	8.0	
F820-4-G5-IR	PLCVVEELFWGASLYGQCSG	8.8	0.6	4.4	0.1	7.5	
F820-4-F2-IR	RLCVLEELFWGASRFRGCSG	11.7	0.6	4.2	0.1	7.4	
F820-4-H8-IR	PLCVLEELHMGALLFGYCSG	16.0	0.6	4.7	0.1	7.3	
F820-4-D7-IR	NLCVVEELFWGASLFPNCSCG	14.5	0.8	5.9	0.1	7.1	
F820-4-B2-IR	QLCVLEELFWGASLFGDCSG	5.0	0.4	2.4	0.2	6.9	
F820-4-C3-IR	HLCVLEELQFWGASLFGQCSG	37.5	1.1	7.5	0.2	6.6	
F820-4-H4-IR	PLCVLEELIYMGALLFGDCYG	21.2	1.1	6.4	0.2	5.9	
F820-4-B10-IR	PLCVLEELFWGLSLDKNCS	7.5	0.7	3.7	0.2	5.6	
F820-4-A5-IR	QLCVLEELFWGASLFGSCSG	5.3	0.8	4.4	0.2	5.2	
F820-4-F6-IR	PLCDLEALFWGESLFGGCSG	5.7	0.6	3.0	0.2	4.9	
F820-4-F1-IR	HLCVLEELFWGTSHFDCSCG	9.1	1.0	4.7	0.2	4.7	
F820-4-A3-IR	DLCLLEELFWGAPLFGLCSCG	5.9	0.8	3.5	0.2	4.5	
F820-4-D1-IR	DLCLLEELFWGVALYGGCSG	25.7	2.3	10.5	0.2	4.5	
F820-4-F5-IR	QLCVLEELYMGASLFGHCSCG	3.7	0.6	2.7	0.2	4.2	
F820-4-F12-IR	HLCVLEDRFWGASLFGPCSCG	11.3	0.6	2.2	0.3	3.5	
F820-4-A11-IR	HLGMEEMFWGVALFRNCSCG	7.6	0.8	2.7	0.3	3.5	
F820-4-E8-IR	PLCVLEQLYMGESLIFYCSCG	8.0	1.2	4.3	0.3	3.5	
F820-4-H3-IR	HLCLLEELFWGEALMWGYCSG	17.5	2.6	9.0	0.3	3.4	

Figure 4D

Clone	Parental/Design	Sequence	Ratios over Background				Comparisons	
			E-Tar	IGfR	IR	IGfR/IR	IR/IGfR	
F820-4-A8-IR		QLCVMEELFWGASLFGYCSCG	6.4	0.7	2.4	0.3	3.4	
F820-4-G1-IR		HLCVLEELFWGASLFGQCSG	3.9	0.6	1.9	0.3	3.4	
F820-4-F3-IR		QLCVLEELFWGASLFGQCSG	9.8	1.3	3.6	0.4	2.9	
F820-4-D6-IR		PLCVLEELFWGASLFGQCSA	5.4	1.2	3.2	0.4	2.6	
F820-4-A1-IR		YLCVQEEELFWGASLFGYCSV	25.5	2.4	6.1	0.4	2.5	
F820-4-H2-IR		HLCVLEELFWGASLFGQCSG	15.9	1.6	4.1	0.4	2.5	
F820-4-F4-IR		HLCVLEELFWGASLFGQCSG	6.8	1.9	4.7	0.4	2.5	
F820-4-B6-IR		QLCDLEELFWGASLFGYCPG	4.1	0.8	1.9	0.4	2.4	
F820-4-B11-IR		HLCVLEELFWGASLFGYCPG	22.2	3.1	7.0	0.4	2.3	
F820-4-H6-IR		QLCVLEELFWGASLFGQCSR	4.1	1.1	2.4	0.5	2.2	
F820-4-H9-IR		PLCVLEELFWGASLFGQCSG	3.1	0.9	1.9	0.5	2.1	
F820-4-D3-IR		QLCDLEELFWGASLFGYCSG	4.6	1.3	2.5	0.5	1.9	
F820-4-C1-IR		QLCVLEELFWGASLFGYCSG	13.0	1.1	2.1	0.5	1.9	
F820-4-D12-IR		QL.DLNTWSGLCLCSVTIVRV	10.4	1.2	2.0	0.6	1.7	
F820-4-B8-IR		DLCVLEELFWGASLFGYCSG	7.2	2.2	3.4	0.6	1.5	
F820-4-C6-IR		HLCVLEELFWGASLFGQCSG	13.9	2.5	2.8	0.9	1.1	
F820-4-C10-IR		HLCVLEELFWGASLFGQCSG	5.3	2.6	2.9	0.9	1.1	
F820-4-D4-IR		QLCVLDALMWGASLFGQCSG	3.5	2.3	2.1	1.1	0.9	
F820-4-E1-IR		QLCVLEELFWGASLFGQCSG	1.6	1.6	1.5	1.1	0.9	
F820-4-B3-IR		HLCVLEELFWGASLFGQCSG	15.9	0.6	5.0	1.2	0.8	
F820-4-D2-IR		QLCVLEELFWGASLFGQCSG	7.8	3.2	2.5	1.3	0.8	
F820-4-C5-IR		HLCVLEELFWGASLFGQCSG	21.5	4.0	2.3	1.8	0.6	

Figure 4D (Con't)

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IC/IR	IC/IR	IR/IC/IR
A6L-3-C4-IR	HLCLVEELFWGASLFGYCSCG	--	--	--	--
A6L-3-D7-IR	DLCLVEERFWGASLFGQCCSG	36.9	1.0	40.5	<0.1 42.5
A6L-3-A1-IR	QLCVLEELHWGASLFGYCSCG	38.6	1.0	40.1	<0.1 40.7
A6L-3-C1-IR	PLCVLEEQFWGASLFGQCCSG	39.6	1.1	44.8	<0.1 40.6
A6L-3-D5-IR	YLCDLEERFWGASLFGQCCSS	37.3	1.0	40.3	<0.1 40.3
A6L-3-A4-IR	HLCLVEERFWGSSQFGFCSCG	42.9	1.1	44.4	<0.1 40.2
A6L-3-D3-IR	HLCLVEELFWGASQFGQCCSG	26.7	1.1	42.2	<0.1 40.2
A6L-3-B1-IR	HLCLVEERFWGASLFGQCCSG	34.6	0.9	36.9	<0.1 39.8
A6L-3-B5-IR	HLCLVEELFWGASLFGQCCSG	33.9	1.0	38.7	<0.1 39.3
A6L-3-B2-IR	HLCLVEERFWGASLFGQCCSG	35.3	1.1	42.4	<0.1 38.6
B6H-4-G12-IR	HLCLVEELFWGASLFGQCCSG	38.1	1.1	42.7	<0.1 37.7
B6C-4-H10-IR	QLCLVEELFWGAASFGQCCSG	31.6	1.1	39.6	<0.1 36.7
B6H-4-G8-IR	HLCLVEEMFWGASLFGQCCSG	38.5	1.1	41.1	<0.1 36.5
A6L-3-D6-IR	HLCLVEELFWGASLFGQCCSR	31.7	1.1	39.7	<0.1 36.2
B6C-4-F1-IR	QLCLVEELFWGASQFGYCSCG	35.5	1.0	37.2	<0.1 36.1
B6H-4-E8-IR	QLCALVEEQFWGASLFGQCCSG	32.9	1.1	38.7	<0.1 35.8
B6C-4-H3-IR	QLCLVEELFWGASLFGQCCSG	37.4	1.2	40.5	<0.1 34.8
B6H-4-G1-IR	HLCLVEEMFWGDSLFGQCCSR	30.2	1.0	35.7	<0.1 34.3
B6C-4-E9-IR	HLCLVEERFWGASLFGQCCSG	34.9	1.2	40.2	<0.1 33.7
B6C-4-F5-IR	QLCELEEVFWGASLFDYCSCG	34.4	1.2	38.8	<0.1 33.2
B6C-4-F11-IR	HLCLVEELFWGASLFGQCCSA	34.7	1.2	39.6	<0.1 32.8
B6C-4-E6-IR	HLCLVEELFWGASLFGQCCSG	34.0	1.2	37.2	<0.1 31.7
B6C-4-E12-IR	HLCLVEELFWGASLFGQCCSG	32.3	1.2	37.4	<0.1 30.6
B6C-4-G10-IR	HLCLVEELFWGASLFGQCCSG	30.9	1.1	33.3	<0.1 30.2
B6C-4-F8-IR	QLCVLEEQFWGASLFGQCCSG	33.0	1.3	40.3	<0.1 30.1
B6C-4-G3-IR	HLCLVEEMFWGASLFGQCCG	26.6	1.1	32.5	<0.1 29.2
20C-3-B7-IR	PLCLVEELVWGASLFGQCCSG	29.5	1.2	32.9	<0.1 28.3

Figure 4E

Clone Design	Sequence	Ratios over Background		Comparisons	
		F-Tag	ICF _{SR}	IR	ICF _{IR} /IR
20C-3-B4-IR	<u>HL</u> CVLEELFMGASLFGYCSCG	--	--	--	--
20C-3-C11-IR	NLCVLEELFMGESLFGQCSG	28.9	1.1	31.1	<0.1
20C-3-C11-IR	HLCVLEEQFMGSLFGYCSR	30.2	1.1	31.0	<0.1
20C-3-B8-IR	HLCFLEEVFMGALFAQCSG	29.4	1.3	35.3	<0.1
20C-3-C10-IR	HLCDLEVLFMGSLFGQCSG	28.5	1.1	31.2	<0.1
20C-3-B6-IR	HLVMEELFMGASLFGQCSG	32.1	1.2	33.6	<0.1
20C-3-B6-IR	HLVLEERFMGASLFGQCSG	29.7	1.2	31.9	<0.1
20C-3-B3-IR	HLVLEEQYMGESLFGYCSG	14.4	1.1	28.3	<0.1
20C-3-A5-IR	PLCVLEEQFMGASLFAVCS	38.7	1.7	43.4	<0.1
20C-3-B11-IR	QLCVLEELFMGESLFAQCLG	22.9	1.1	27.6	<0.1
20C-3-B11-IR	HLCVLEELFMGSLFGHCSG	30.0	1.3	32.7	<0.1
20C-3-B3-IR	HLCVLEELVMGASLFGFCSCG	29.3	1.2	31.2	<0.1
20C-3-C12-IR	LLCVLEEQFMGASLFGQCSG	29.6	1.3	31.8	<0.1
20C-3-C3-IR	RLCVLEELFMGESLFGQCSG	30.1	1.2	30.1	<0.1
20C-3-C2-IR	HLCVLEEMFMGASLFGNCSG	29.9	1.3	29.8	<0.1
20C-3-A11-IR	ELCFLEELFMGASLFGQCSG	25.9	1.2	27.4	<0.1
20C-3-A4-IR	HLCVLEELFMGASLYGQCS	27.2	1.2	27.5	<0.1
20C-3-A6-IR	HLCVLEELFMGASLFAQCPG	26.1	1.2	27.5	<0.1
20C-3-A4-IR	NLCVLEELFMGASEFGQCSG	34.5	1.7	39.1	<0.1
20C-3-A9-IR	PLCVLEEQLMGASLFRYCSG	29.7	1.3	29.3	<0.1
20C-3-C5-IR	HLCVLEEQFMGVALFGNCSG	33.5	1.7	37.7	<0.1
20C-3-B1-IR	HLCVLEEQIMGASLFGQCSG	30.2	1.2	26.7	<0.1
20C-3-A10-IR	HLCVLEERFMGALFGQCTA	29.0	1.3	28.5	<0.1
20C-4-F1-IR	HLCDLEELFMGASLFGQCSG	29.1	1.4	29.5	<0.1
20C-4-E1-IR	QLCVLEELFMGTSLFAQCSG	28.3	1.4	29.7	<0.1
20C-3-B12-IR	QLCGLEELFMGASLFGYCSA	27.0	1.3	25.8	<0.1
20C-3-A8-IR	HLCVLEELFMGASLFGQCSS	21.1	1.1	21.2	0.1
20C-3-A7-IR	PLCVLEELFMGASQFGQCSG	21.9	1.3	23.0	0.1
20C-4-E10-IR	HLCVLEEQFMGASLFGYCSG	35.2	2.2	38.0	0.1

Figure 4E (Con't)

Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGF _S R	IR	IGF _R /IR	IR/IGF _R	
20C-3-A1-IR	<u>HLCVLEELFWGASLFGYCSG</u>	--	--	--	--	--	--
20C-3-A1-IR	<u>RLCALLEELFWGASLFGQCSG</u>	21.0	1.1	17.6	0.1	16.6	
20C-3-C1-IR	<u>HLCVLEELFWGAAALFHQCSG</u>	30.6	1.4	21.9	0.1	16.1	
A6L-3-D2-IR	<u>RLCVLEELFWGASLFGQCSG</u>	7.0	1.1	14.9	0.1	14.1	
B6C-4-G12-IR	<u>QLCVLEELFWGSSRLGYCSG</u>	31.1	2.5	33.5	0.1	13.6	
B6H-4-F9-IR	<u>DLCVLEELFWGASLFGQCSG</u>	39.3	3.6	43.1	0.1	12.1	
B6C-4-E3-IR	<u>QLCLLEELFWGGSLLFGQCSG</u>	34.6	5.3	40.0	0.1	7.6	
20C-3-B10-IR	<u>HLCVLEELFWGTSLFGQCSG</u>	29.9	16.9	31.7	0.5	1.9	
20C-3-A3-IR	<u>RLCVLEELVWGASLFDQCSR</u>	28.4	19.1	25.3	0.8	1.3	

Figure 4E (Con't)

Clone	Parental/Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGfsR	IR	IGfR/IR	IR/IGfR	
		HLGVLEELFMGASLFGYCSG	39.1	1.8	27.7	0.1	15.4	
	F815-4-D10-IGFR	PLQALCEKFFGAWMFGYCSG	31.2	13.9	1.0	13.9	0.1	
	F815-4-H11-IGFR	HLQVLCELFPGVYLFGYCSG	27.2	19.2	1.7	11.3	0.1	
	F815-4-C8-IGFR	PLFDLCELFPGASLSGYCYG	35.4	17.4	1.6	10.9	0.1	
	F815-4-E8-IGFR	HL*ALCELFPGVMSFGYCVG	29.5	16.9	1.7	9.9	0.1	
	F815-4-E11-IGFR	QLGVLCMFGGAFLRGYCQG	36.6	25.7	2.7	9.5	0.1	
	F815-4-A7-IGFR	HLQDLCELFPGAYLFGYCSG	29.6	16.0	3.8	4.2	0.2	
	F815-3-D3-IGFR	QLQVLCELFPGAVSLRLLLM	33.7	3.5	1.0	3.5	0.3	
	F815-4-F7-IGFR	PLGVLCEDFGGAFRFGYCSG	33.6	18.9	9.9	1.9	0.5	
	F815-4-A9-IGFR	PL*GLCELFPGASLFGYCSS	7.5	1.7	2.3	0.7	1.4	
	F815-4-B12-IGFR	DLRVLCELFGAYVLGYCSE	35.1	3.7	12.6	0.3	3.4	

Figure 5

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGfsR	IR	IGfsR/IR	IR/IGfsR
R20α-3-20A4-IR	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20β-4-A7-IR	EIEAEWGRVRCLVYGRGVGG	50.2	1.6	23.1	0.1	14.4
R20β-4-D8-IR	EIEAEWGRVRCLVYGRGVGG	44.2	1.3	24.0	0.1	18.5
	WLDQEWAWVQCEVYGRGCPs	44.8	1.4	24.2	0.1	17.3

Figure 6A

Clone	Par ntal/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	ICFSR	IR	ICFR/IR	IR/ICFR
D815-4-A8-IR		<u>WLDQEWAMVQCEVYGRGCP</u> S	44.8	1.4	24.2	<0.1	17.3
D815-4-A8-IR		WLDLEMAQVQCEVYGRGCPS	48.0	1.0	48.4	<0.1	48.4
D815-4-D10-IR		WLDQEWAMVQCEVFGRCCPS	49.2	1.0	48.2	<0.1	48.2
D815-4-D9-IR		WLDQEWQVQVQCVYGRGCTS	47.5	1.0	48.0	<0.1	48.0
D815-4-A11-IR		RLDEEMARVQCEVMWGRCRS	47.9	1.0	48.0	<0.1	48.0
D815-4-E12-IR		WLEQEWAMIQCEVYGRGCPS	49.0	1.0	47.6	<0.1	47.6
D815-4-B7-IR		WLEQEWAMVQCEVYGRGCPS	45.4	1.0	47.2	<0.1	47.2
D815-4-D11-IR		WLEDEEWMIQCKVYGRGCPA	49.5	1.0	47.0	<0.1	47.0
D815-4-D12-IR		WLEQEWAMVQCEVYGRGCCS	48.1	1.0	46.6	<0.1	46.6
D815-4-F8-IR		WLDQEWAMIQCEVYGRGCPA	47.8	1.0	46.4	<0.1	46.4
D815-4-A9-IR		SLDQEWAMVQCEVYGRGCPS	47.7	1.0	45.8	<0.1	45.8
D815-4-E9-IR		WLEQEWQVRLVYGRGCPP	47.8	1.0	45.8	<0.1	45.8
D815-4-B10-IR		WLDQEWAMVQCEVYGRGCPY	49.0	1.0	45.6	<0.1	45.6
D815-4-H8-IR		WLDQEWAGVLCVYGRGCPS	49.0	1.0	45.6	<0.1	45.6
D815-4-E10-IR		SLDKEMEWLQCVYGRGCPS	47.0	1.0	45.6	<0.1	45.6
D815-4-D7-IR		WLEQEWAMVQCEVYGRGCRS	44.5	1.0	45.4	<0.1	45.4
D815-4-G9-IR		WLEQEWAMVQCAVYGRGCCS	44.2	1.0	44.2	<0.1	44.2
D815-4-G12-IR		WLDQEWALVQCEVYGRGCPS	44.3	1.0	43.7	<0.1	43.7
D815-4-E11-IR		WLDQEWAMVQCEVYGRGCPS	45.5	1.0	43.0	<0.1	43.0
D815-4-H7-IR		WLEQEWAMVQCEVYGRGCAS	46.2	1.0	43.0	<0.1	43.0
D815-4-F12-IR		WLDQEWAMVECEVYGRGCPS	47.2	1.0	42.6	<0.1	42.6
D815-4-E8-IR		WLDQEWAMVECVYGRGCPS	47.9	1.0	42.6	<0.1	42.6
D815-4-F9-IR		QLDQEWAMVLCVYGRGCPS	46.4	1.0	41.8	<0.1	41.8
D815-4-A10-IR		WLDHE*AMVQCEVYGRGCPS	47.3	1.0	41.2	<0.1	41.2
D815-4-C7-IR		QLEQEWAMVRCEVYGRGCCS	37.7	1.0	40.0	<0.1	40.0
D815-4-H10-IR		WLDQEWAMVQCVYGRGCLS	47.0	1.0	39.8	<0.1	39.8
D815-4-C9-IR		WLDQEWAMVRCEVYGLGCPS	44.2	1.0	39.8	<0.1	39.8
D815-4-F11-IR		WLDQEWAMVKCEL YGRGCPS	40.4	1.0	39.2	<0.1	39.2
D815-4-H12-IR		WLEQEWAMVQCEVYGRGCLS	45.4	1.0	38.6	<0.1	38.6
D815-4-A7-IR		SLDQEWAMVQCEVYGRGCLS	37.3	1.0	37.3	<0.1	37.3
D815-4-H11-IR		WLDHEAMVQCEVYGRGCTS	2.4	1.0	37.2	<0.1	37.2
D815-4-F7-IR		WLDVEMAMVQCEVYGRGCPS	32.4	1.0	34.7	<0.1	34.7

Figure 6B

Clone	Sequence
Parental/Design	
D815-4-G8-IR	<u>WLDPQEWAMVQCEVYGRGCP</u> S
D815-4-G7-IR	<u>QLDPQEWARVRCEVWGRG</u> CS
D815-4-G11-IR	WLDPLEWAQVQCKVYGRGCP
D815-4-E7-IR	WLDEEWAMVQCEVWGRGCAF
D815-4-A12-IR	WLDPREWAQVQCEVYGRGCLS
D815-4-B11-IR	WLDAEWEMVQCEVYGRGCRP
D815-4-D8-IR	SLDREWAYVQCEVYGRGCS

Ratios over Background				Comparisons	
F-Tag	ICFSR	IR	ICFR/IR/ICFR		
--	--	--	--	--	--
27.8	1.0	33.6	<0.1	33.6	
34.7	1.0	32.3	<0.1	32.3	
30.7	1.0	28.6	<0.1	28.6	
33.0	1.0	26.4	<0.1	26.4	
28.4	1.0	19.0	0.1	19.0	
22.1	1.0	18.8	0.1	18.8	
20.8	1.0	14.6	0.1	14.6	

Figure 6B (Con't)

Clone Parental/Design	Sequence	Ratios over Background			Comparisons	
		F-Tag	IGFSR	IR	IGFIR/IR	IR/IGFIR
D820-3-H2-IR	WLDQEWAMVQCEVYGRGCPSS	44.8	1.4	24.2	0.1	17.2
D820-3-H2-IR	RLDLEWANIQCEVYGRGCPSS	23.9	1.0	40.0	<0.1	40.0
D820-3-C4-IR	WLEQEWAMVQCEVYGRGCCSS	31.0	1.0	39.5	<0.1	39.5
D820-3-C3-IR	WLEQEWILVECEVYGRGCPT	35.2	1.0	39.4	<0.1	39.4
D820-3-G6-IR	WLEQEWAMVQCEVWGRGCPSS	33.8	1.0	38.8	<0.1	38.8
D820-3-D2-IR	WLDQEWEMIQCEVYGRGCPL	35.6	1.0	37.8	<0.1	37.8
D820-3-D3-IR	LQDEWMAQIECEIYGRGCPSS	34.8	1.0	37.7	<0.1	37.7
D820-3-B5-IR	ALQEWAMVQCEVYGRGCHF	34.1	1.0	37.1	<0.1	37.1
D820-3-E2-IR	C?EQEWGLVQCEVYGRGCPSS	34.4	1.0	37.0	<0.1	37.0
D820-3-B3-IR	WLEQEWAYVQCEVYGRGCPSS	33.6	1.0	36.7	<0.1	36.7
D820-3-B6-IR	WLEHEMWAMVQCEVWGRGCPY	31.2	1.0	36.6	<0.1	36.6
D820-3-D4-IR	WLEQEWAEVRCEVYGRGCPR	32.0	1.0	36.2	<0.1	36.2
D820-3-C2-IR	?LEQEWAMVQCEVYGRGCPSS	33.7	1.0	35.6	<0.1	35.6
D820-3-F6-IR	WLEQEWAGIQCKVYGRGCPSS	30.8	1.0	35.2	<0.1	35.2
D820-3-D5-IR	RLEQEWAMVQCEVWGRGCLP	30.5	1.0	34.8	<0.1	34.8
D820-3-F5-IR	QLDHEWAGIQCEVWGRGCPSS	29.8	1.0	34.6	<0.1	34.6
D820-3-H3-IR	WLEQEWAMVQCEVYGRGCPSS	30.2	1.0	33.8	<0.1	33.8
D820-3-G2-IR	SLEQEWAMVQCEVYGRGCPPI	31.3	1.0	33.0	<0.1	33.0
D820-3-H6-IR	WLEQEWMDQVLCVYGRGCPY	30.3	1.0	32.2	<0.1	32.2
D820-3-F3-IR	WLEQEWAMVQCEVYGRGCPA?	28.6	1.0	30.7	<0.1	30.7
D820-3-B4-IR	WMDQEWAMVQCEVYGRGCPSS	33.1	1.0	30.5	<0.1	30.5
D820-3-C5-IR	QLDQEWAMIQCEVYGRNCRT	29.1	1.0	30.3	<0.1	30.3
D820-3-F4-IR	TLEQEWAMVQCEVYGRGCLS	25.9	1.0	29.5	<0.1	29.5
D820-3-H5-IR	RLEQEWAMVQCEVWGRGCLS	26.3	1.0	28.6	<0.1	28.6
D820-3-A6-IR	WLDQEWAMVQCEVYGRGCPA	24.8	1.0	26.0	<0.1	26.0
D820-3-A2-IR	WLDQEWAMVQCEVYGRGCPA	23.7	1.0	25.6	<0.1	25.6
D820-3-G5-IR	WLEQEWAMVQCEVYGRGCPSS	22.6	1.0	25.0	<0.1	25.0
D820-3-G3-IR	RLEQEWAMVQCEVYGRGCPSS	22.2	1.0	23.9	<0.1	23.9
D820-3-E3-IR	WLEQEWAMVQCEVYGRGCPSS	20.6	1.0	22.7	<0.1	22.7

Figure 6C

Clone	Sequence	Ratios over Background				Comparisons	
Parental/Design		F-Tag	ICFSR	IR	ICFR/IR	IR/ICFR	
D820-3-E5-IR	WLDQEWAMVQCEVYGRGCPS	44.8	1.4	24.2	0.1	17.2	
D820-3-D1-IR	WLEQEWMTWQCEVYGCQCPS	25.9	1.0	22.6	<0.1	22.6	
D820-3-E1-IR	WLEKEMAGVQCEIYGRGCPS	27.3	1.0	22.4	<0.1	22.4	
D820-3-F1-IR	WLEBEMAWVRCEVYGRGCQS	22.4	1.0	21.9	<0.1	21.9	
D820-3-B2-IR	WLEHMAQIQCELYGRGCTY	22.0	1.0	21.0	<0.1	21.0	
D820-3-A3-IR	ALBEBEMAWQCEVYGRGCPS	13.1	1.0	18.4	0.1	18.4	
D820-3-H4-IR	WLEQEWAGVQCEVYGRGCPS	23.5	1.0	18.4	0.1	18.4	
D820-3-G1-IR	WLDDEMAQIQCEIYGRGCQS	25.6	1.0	17.5	0.1	17.5	
D820-3-C1-IR	QLEEBEMAGVQCEVYGRGCPS	14.5	1.0	16.3	0.1	16.3	
D820-3-A1-IR	WLEQEWLLVQCGVYGRGCPS	27.8	1.0	13.9	0.1	13.9	
D820-3-A5-IR	WLDQEWAMIQCEVYGRGCPS	14.7	1.0	12.8	0.1	12.8	
D820-3-H1-IR	WLEQEWAGVQCEVYGRGCPS	6.4	1.0	6.3	0.2	6.3	
D820-3-A4-IR	WLDQEWALIQCEVYGRGCPS	13.7	1.0	6.2	0.2	6.2	
D820-4-E12-IR	SLDEEMAGVLCVYGRGCPF	6.0	1.0	4.3	0.2	4.3	
D820-4-B12-IR	SVDQLEWLMCHFQGRVCP	34.9	9.0	10.9	0.8	1.2	
	WLEQERAWIWCETIQSGCRA	32.2	8.6	1.0	8.6	0.1	

Figure 6C (Con't)

Clone	Parental/Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGFR	IR	IGFR/IR	IR/IGFR	
		WLDQEWAMVQCEVYGRGCP	44.8	1.4	24.2	0.1	17.3	
D820-3-D5-IGFR		WVNQALGVQSDVQGRQCQ	29.6	3.8	1.0	3.8	0.3	
D820-3-E4-IGFR		LLDHEMPWVGCEVCGRGLS	27.1	3.2	1.0	3.2	0.3	
D820-3-C5-IGFR		WLHQELAWVRGEGYPRGRS	25.0	3.1	1.0	3.1	0.3	
D820-3-F4-IGFR		WLGHDWAMIQCEVYGLGCP	3.9	2.7	1.0	2.7	0.4	
D820-3-F6-IGFR		WIDQEGVRVQCEA*GRAFPS	26.7	2.6	1.0	2.6	0.4	
D820-3-G4-IGFR		WRDEEWAMVQGVVQGRWPA	3.8	2.6	1.0	2.6	0.4	
D820-3-E2-IGFR		RLGVESWFWQKRYGRDSTS	15.3	2.6	1.0	2.6	0.4	
D820-3-G6-IGFR		WLAQGMAGVQCVVYGRGCRN	20.3	2.4	1.0	2.4	0.4	
D820-4-E11-IGFR		WLEEE*AGIQCV?GRGCP	12.6	1.0	3.0	0.3	3.0	
D820-4-H11-IGFR		WLDQEWEMVQCEVWGRGCLS	8.1	1.0	4.6	0.2	4.6	
D820-4-D11-IGFR		RLEQEWALIQCEVYGRGCP	4.5	1.0	5.3	0.2	5.3	
D820-4-A8-IGFR		WLEEEWAQVQCVVYGRGCAS	3.2	1.0	5.5	0.2	5.5	
D820-4-F9-IGFR		WLDLE*EWLQCEVYGRGCAT	9.4	1.0	5.8	0.2	5.8	
D820-4-C8-IGFR		WLEQEWVQVRCEVYGRGCP	11.6	1.0	5.9	0.2	5.9	
D820-4-D9-IGFR		WLEEEWAQVQCEVYGRGCP	10.1	1.0	8.9	0.1	8.9	
D820-4-D7-IGFR		WLDQEWARVQCEVWGRGCTY	34.1	3.5	33.4	0.1	9.5	
D820-4-H9-IGFR		YLD?EWAMVQCEVYGLGCQS	18.4	1.0	10.1	0.1	10.1	
D820-4-E10-IGFR		WLDVE*AMVQCEVWGRGCP	26.7	2.6	27.0	0.1	10.4	
D820-4-E7-IGFR		WLEQEWER?QCEVYGRGCP	31.9	3.0	32.2	0.1	10.7	
D820-4-H8-IGFR		WLEEEWAQVQCEVYGRGCLS	16.1	1.0	11.7	0.1	11.7	
D820-4-A11-IGFR		WLDQEWAMIQCEVYGRGCP	8.0	1.0	12.5	0.1	12.5	
D820-4-C9-IGFR		?LEHEWAQIQCEV?GRGCQS	19.6	1.0	14.9	0.1	14.9	
D820-4-E9-IGFR		WL?QEWAMIQCEVYGRGCP	19.3	1.0	17.3	0.1	17.3	
D820-4-B10-IGFR		WLD?EWAMVQCEVYGRGCP	19.3	1.0	21.5	<0.1	21.5	
D820-4-F10-IGFR		GLEQGCPRWGLEVQCRGCP	27.8	1.0	25.7	<0.1	25.7	
D820-4-B9-IGFR		WLEEEWAQVQCEVYGHGCP	31.7	1.0	26.5	<0.1	26.5	
D820-4-G8-IGFR		WLDQEWAMQIQCEVYGRGCSS	25.6	1.0	29.3	<0.1	29.3	

Figure 6D

Clone	Parental/Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR	
		WLDQEWAMVQCEVYGRGCP	44.8	1.4	24.2	0.1	17.3	
	D820-4-G9-IGFR	WLDQEWAMVQCEVWGRGCP	36.8	1.0	29.6	<0.1	29.6	
	D820-4-C10-IGFR	WLDLEWEFVQCEVYGRGCP	32.6	1.0	31.3	<0.1	31.3	
	D820-4-A9-IGFR	WLEQEWASVQCEVYGRGCP	20.4	1.0	31.4	<0.1	31.4	
	D820-4-B8-IGFR	WLDLEWEQIKCKVYGRGCP	31.1	1.0	32.7	<0.1	32.7	
	D820-4-F8-IGFR	WLEQEWAMVQCEVYGRGCP	28.3	1.0	32.9	<0.1	32.9	
	D820-4-H7-IGFR	WLEQEWALVLCVYGRGCP	34.1	1.0	32.9	<0.1	32.9	
	D820-4-E8-IGFR	WLEQEWAMVQCEVWGRGCS	26.6	1.0	33.2	<0.1	33.2	
	D820-4-G10-IGFR	WLEQEWAMVQCEVYGRGCP	37.5	1.0	33.2	<0.1	33.2	
	D820-4-D10-IGFR	WLEQEWAMVQCEVYGRGCP	36.6	1.0	33.5	<0.1	33.5	
	D820-4-D8-IGFR	WLEQEWAMVQCEVWGRGCP	23.7	1.0	34.6	<0.1	34.6	
	D820-4-A10-IGFR	WLDQEWAMVQCEVWGRGCP	29.4	1.0	35.5	<0.1	35.5	
	D820-4-B7-IGFR	PLEHEWAMVQCEVYGRGCR	35.4	1.0	36.9	<0.1	36.9	
	D820-4-E12-IGFR	SLEQEWAMVQCEVYGRGCP	37.0	1.0	37.0	<0.1	37.0	
	D820-4-H10-IGFR	WLDQEWAMVQCEVWGRGCP	36.8	1.0	37.1	<0.1	37.1	
	D820-4-F12-IGFR	SLDKEWAMVQCEVYGRGCP	36.9	1.0	37.3	<0.1	37.3	
	D820-4-F7-IGFR	LGDQEWAMVQCEVWGRGCP	34.4	1.0	37.5	<0.1	37.5	
	D820-4-G12-IGFR	WLEEWAMVQCEVYGRGCP	30.3	1.0	37.8	<0.1	37.8	
	D820-4-D12-IGFR	WLEEWAMVQCEVWGRGCP	37.2	1.0	38.6	<0.1	38.6	
	D820-4-A12-IGFR	CLDQEWAMVQCEVYGRGCP	30.4	1.0	39.3	<0.1	39.3	
	D820-4-C12-IGFR	QLELEWAMVQCEVWDRGCP	37.1	1.0	39.6	<0.1	39.6	
	D820-4-A7-IGFR	RLEQEWAMVQCEVYGRGCR	35.4	1.0	40.8	<0.1	40.8	
	D820-4-B12-IGFR	SLEHEWAMVQCEVYGRGCP	36.2	1.0	41.4	<0.1	41.4	

Figure 6D (Con't)

Clone	Parental/Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGFSR	IR	IGFR/IR		
		IR/IGFR						
		WLDQENAWVQCEVYGRGCP	44.8	1.4	24.2	<0.1	17.3	
	B6-4-G12-IR	WLDQENAWIQCEVYGRGCPP	4.4	1.0	6.9	0.1	7.1	
	B6-3-A11-IR	WLDQENAVRCEVYGRGCP	7.3	1.0	6.3	0.2	6.3	

Figure 6E

	Sequence	HIR affinity mol/l
J228	HPPLEHLKAFLL-NH ₂	2.4*10 ⁻⁵
J229	APTFYAWFNQQT-NH ₂	2.4*10 ⁻⁶
S122	HPTSKEIYAKLLK	9.3*10 ⁻⁶
S123	HPSTNQMLMKLFK	1.6*10 ⁻⁵
S124	HPPLSELKLFLIKK	2.3*10 ⁻⁵

Figure 7

J-nr	Sequence	HIR affinity mol/l
J101	ACVWPTYWNCG	$5.0 \cdot 10^{-6}$
J103	Ac-CVWPTYWNCG	$3.0 \cdot 10^{-5}$
J104	Bz-CVWPTYWNCG	$3.2 \cdot 10^{-5}$
J105	Ac-ACVWPTYWNCG	$4.5 \cdot 10^{-5}$
J109	ACVWPTYWACG	$2.0 \cdot 10^{-5}$
J110	ACVWPTYANCG	$2.4 \cdot 10^{-5}$
J111	ACVWPTAWNCG	$3.1 \cdot 10^{-5}$
J112	ACVWPAYWNCG	$3.3 \cdot 10^{-5}$
J113	ACVWATYWNCG	$5.5 \cdot 10^{-5}$
J115	ACAWPTYWNCG	$2.7 \cdot 10^{-6}$
J116	AAVWPTYWNAG	$3.4 \cdot 10^{-5}$
J117	ASVWPTYWNSG	$2.9 \cdot 10^{-5}$
J118	ACPYNW/TWCG	$2.9 \cdot 10^{-5}$
J119	ACVWPTYWnCG	$3.2 \cdot 10^{-5}$
J120	ACVWPTYwNCG	$3.4 \cdot 10^{-5}$
J121	ACVWPTYWNCG	$1.8 \cdot 10^{-5}$
J122	ACVWPIYWNCG	$5.1 \cdot 10^{-5}$
J123	ACVWPtYWNCG	$2.5 \cdot 10^{-5}$
J124	ACVwPTYWNCG	$2.0 \cdot 10^{-5}$
J125	ACvWPTYWNCG	$1.8 \cdot 10^{-5}$
J127	acvwptywncg	$4.4 \cdot 10^{-5}$
J128	gcnwytpwvca	$5.3 \cdot 10^{-5}$
J130	AEVWPTYWN(Dpr)G	$1.9 \cdot 10^{-5}$
J131	ACdWPTYWNCG	$5.5 \cdot 10^{-5}$
J132	AC(Leu)WPTYWNCG	$4.5 \cdot 10^{-6}$
J133	AC(dLeu)WPTYWNCG	$2.8 \cdot 10^{-5}$
J134	AC(Ile)WPTYWNCG	$7.4 \cdot 10^{-6}$
J135	AC(dIle)WPTYWNCG	$2.9 \cdot 10^{-5}$
J136	AC(Met)WPTYWNCG	$7.5 \cdot 10^{-6}$

FIGURE 8



J137	AC(dMet)WPTYWNCG	$2.5 \cdot 10^{-5}$
J138	AC(Abu)WPTYWNCG	$7.8 \cdot 10^{-5}$
J139	AC(dAbu)WPTYWNCG	$2.1 \cdot 10^{-5}$
J140	AC(Nva)WPTYWNCG	$3.6 \cdot 10^{-6}$
J141	AC(dNva)WPTYWNCG	$3.0 \cdot 10^{-5}$
J142	AC(tBuG)WPTYWNCG	$3.2 \cdot 10^{-5}$
J143	AC(diBuG)WPTYWNCG	$3.8 \cdot 10^{-5}$
J144	AC(Phe)WPTYWNCG	$5.1 \cdot 10^{-6}$
J145	AC(dPhe)WPTYWNCG	$5.7 \cdot 10^{-5}$
J146	AC(Cha)WPTYWNCG	$2.2 \cdot 10^{-5}$
J147	AC(dCha)WPTYWNCG	$1.7 \cdot 10^{-5}$
J148	AC(Nal(1))WPTYWNCG	$5.8 \cdot 10^{-6}$
J149	AC(dNal(1))WPTYWNCG	$2.0 \cdot 10^{-5}$
J150	AC(Acy)WPTYWNCG	$2.0 \cdot 10^{-5}$
J151	ACVWPT(Hyp)WNCG	$2.2 \cdot 10^{-4}$
J154	ACVWPT(Nal2)WNCG	$8.2 \cdot 10^{-5}$
J155	ACVWPT(MetO ₂)WNCG	$1.9 \cdot 10^{-4}$
J157	ACVWPT(Cha)WNCG	$1.2 \cdot 10^{-4}$
J160	ACVWPT(Ser)WNCG	$1.8 \cdot 10^{-4}$
J162	ACVWPT(Thi)WNCG	$2.5 \cdot 10^{-4}$
J163	ACVWPT(dSer)WNCG	$5.0 \cdot 10^{-5}$
J166	ACVWPT(dCha)WNCG	$7.5 \cdot 10^{-5}$
J170	ACVWPT(dPhe)WNCG	$1.4 \cdot 10^{-4}$
J171	ACVWPT(Thr)WNCG	$7.7 \cdot 10^{-4}$
J174	ACVWPT(Phe)WNCG	$4.5 \cdot 10^{-5}$
J176	ACVWPT(dThr)WNCG	$2.8 \cdot 10^{-5}$
J180	ACVWPTYW d CG	$5.6 \cdot 10^{-5}$
J182	ACVWPT d WNCG	$2.7 \cdot 10^{-5}$
J183	ACVWP d YWNCG	$3.3 \cdot 10^{-5}$
J184	ACVW d TYWNCG	$6.2 \cdot 10^{-5}$

Figure 8 (Con't)



J185	ACV d PTYWNCG	$3.4 \cdot 10^{-5}$
J186	AC d WPTYWNCG	$3.5 \cdot 10^{-5}$
J187	ACVWTYWNPCG	$4.3 \cdot 10^{-5}$
J188	ACVWTYWPNCG	$3.0 \cdot 10^{-5}$
J189	ACVWTPYWNCG	$3.1 \cdot 10^{-5}$
J190	ACVWTPYWNCG	$2.6 \cdot 10^{-5}$
J191	ACVPWTYWNCG	$3.0 \cdot 10^{-5}$
J192	ACPWTYWNCG	$4.2 \cdot 10^{-5}$
J193	ACWPTYWNVCG	$4.8 \cdot 10^{-5}$
J194	ACPTYWNVWCG	$4.2 \cdot 10^{-5}$
J195	ACTYWNVWPCG	$3.3 \cdot 10^{-5}$
J196	ACYWNVWPTCG	$2.4 \cdot 10^{-5}$
J197	ACWNVWPTYCG	$2.9 \cdot 10^{-5}$
J198	ACNVWPTYWCG	$4.2 \cdot 10^{-5}$
J199	ACVWPCG	$4.7 \cdot 10^{-5}$
J200	CVWPTYWNCG	$5.5 \cdot 10^{-5}$
J201	ACWWPTYWNCG	$6.8 \cdot 10^{-6}$
J202	ACEWPTYWNCG	$4.6 \cdot 10^{-6}$
J203	ACRWPTYWNCG	$5.8 \cdot 10^{-6}$
J204	ACQWPTYWNCG	$9.2 \cdot 10^{-6}$
J205	ACGWPTYWNCG	$4.4 \cdot 10^{-6}$
J207	cyclo-Valeroyl-AWPTYWNCG	$5.5 \cdot 10^{-5}$
J208	cyclo-Toluy- AWPTYWNCG	$7.6 \cdot 10^{-5}$
J209	cyclo-Acetyl- AWPTYWNCG	$7.7 \cdot 10^{-5}$
J210	(WPTYWNCG) ₂	$5.3 \cdot 10^{-5}$
J211	(AWPTYWNCG) ₂	$7.9 \cdot 10^{-6}$
J212	ACA(Bpa)PTYWNC GK(biotin	$1.8 \cdot 10^{-5}$
J213	ACAWPTY(Bpa)NC GK(biotin	$1.8 \cdot 10^{-5}$
J214	GCAWPTYWNCG	$1.4 \cdot 10^{-6}$
J215	NCAWPTYWNCG	$9.0 \cdot 10^{-6}$

Figure 8 (Con't)



J216	VCAWPTYWNCG	$2.8 \cdot 10^{-6}$
J227	SFYEAHQLLGV-NH ₂	$6.4 \cdot 10^{-6}$
J228	HPPLEHLKAFLL-NH ₂	$2.4 \cdot 10^{-5}$
J229	APTFYAWFNQQT-NH ₂	$2.4 \cdot 10^{-6}$
S122	HPTSKEIYAKLLK	$9.3 \cdot 10^{-6}$
S123	HPSTNQMLMKLFK	$1.6 \cdot 10^{-5}$
S124	HPPLSELKLFLIKK	$2.3 \cdot 10^{-5}$

Figure 8 (Con't)

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	ICFsR	IR	ICF/IR IR/ICFR
H5 Parental	<u>LCQSLGVTYPGWL</u>AGMCA	--	1.2	--	--
H5-3-JBA5-IGFR	LCQSWGVRIQWLAGLCP	31.9	16.3	--	--
H5-3-E1A11-IGFR	VCQSLGITDGLCAGMGA	21.3	8.0	--	--
H5-3-E4B10-IGFR	LCQSLGLTHPGFEAMLCA	29.7	7.8	--	--
H5-3-E4C10-IGFR	LCQNFQVTPGCFYGMFA	24.3	6.1	--	--
H5-3-JBB6-IGFR	PCQRLGPTHLCLAGMFA	40.2	5.4	--	--
H5-3-E4A9-IGFR	LCQSSGLSFLGCLGWWA	27.7	4.3	--	--
H5-3-E2A12-IGFR	LCQSLGFTPLDMLACWFE	27.2	4.2	--	--
H5-3-E4A12-IGFR	VCQGLGVECPGMFAGMWA	27.9	3.9	--	--
H5-3-E1F9-IGFR	PCQSLGLTCSGMFEGMGA	18.6	3.5	--	--
H5-3-E4F11-IGFR	LCQGWGIRIGMLVGRM	28.4	3.3	--	--
H5-3-E4A11-IGFR	LMQSVGIKYPGGLAGWLA	31.0	3.0	--	--
H5-3-E4G7-IGFR	QMQSLGVTCPGSWAELCA	26.2	2.2	--	--
H5-3-E1B9-IGFR	LCQSLGVTYMEGLAWLCA	20.0	2.1	--	--

Figure 9A

Clone	Sequence	Ratios over Background			Comparisons	
		E-Tig	IGFSR	IR	IGFSR/IR	IR/IGFSR
JBA5 Parental	LCQSWGVRIGWLAGLCP	31.5	20.6	1.0	20.6	<0.1
JBA5-4-2C12-IGFR	LCQSWGVRIGWLAGLCP	46.8	41.5	1.0	41.5	<0.1
JBA5-2-1F9-IGFR	LCESWGVRIGWLAGLCP	48.1	39.5	1.0	39.5	<0.1
JBA5-2-1E10-IGFR	LCQSWGVRIGWLVGLCP	42.5	39.5	1.1	35.9	<0.1
JBA5-4-2A11-IGFR	LCQSWGVRIGWLAGLCP	44.1	40.2	1.2	33.5	<0.1
JBA5-3-2A3-IGFR	LCQSWGVRIGWLVGLCP	34.7	33.3	1.0	33.3	<0.1
JBA5-4-2A9-IGFR	LCQSWGVRIGWLTGLCP	34.6	33.1	1.0	33.1	<0.1
JBA5-1-1B6-IGFR	MCQSWDVRIIGRLGGQCP	39.6	31.4	1.0	31.4	<0.1
JBA5-4-2B9-IGFR	LCQGWVRIIGQLAGLCP	39.6	22.3	1.0	22.3	<0.1
JBA5-1-1H7-IGFR	LCQSWGVRIGWLAGLCP	24.9	22.6	1.2	18.8	0.1
JBA5-3-2C3-IGFR	LCQSWDVRIIGWVAGLCP	35.5	15.3	1.1	13.9	0.1
JBA5-1-1G7-IGFR	LCQSWDARIIGWLAGLCP	26.2	14.8	1.5	9.9	0.1
JBA5-2-1E9-IGFR	LCLG*DVRIIGLLAGLCP	39.4	4.5	1.0	4.5	0.2
JBA5-2-1D12-IGFR	L*KSMDVRSGLMAGLCP	42.2	2.2	1.0	2.2	0.5

Figure 9B

Clone	Design	Sequence	Ratios over Background					Comparisons	
			E-Tag	IGF _{SR}	IR	IGF _{IR} /IR	IR/IGF _{IR}		
		LCQSWGVRIGWLAGLCP	--	--	--	--	--		
	JBA5-4-G12-IR	LCQSWDACTQMLVGLSP	37.5	3.0	1.4	2.1	0.5		
	JBA5-4-G3-IR	LCRSWEECIGMLVGPPQ	4.5	2.5	1.1	2.3	0.4		
	JBA5-4-G1-IR	LCQSWGECIDRLVGQGA	32.0	3.2	1.3	2.5	0.4		
	JBA5-3-B1-IR	LCQSWGVRIGWLAGLCP	29.4	6.8	1.2	5.7	0.2		
	JBA5-3-C1-IR	LCQGMVAVHIGQLAGLCP	36.3	7.5	1.1	6.8	0.1		
	JBA5-3-A6-IR	LCQGMGVHIGRLAGLCP	28.0	7.4	0.7	10.6	0.1		
	JBA5-3-A2-IR	LCQSWGVRIGWLAGLCP	10.2	4.8	0.4	12.0	0.1		
	JBA5-3-B7-IR	LCQSWGVIHIGRLAGLCP	39.2	15.2	1.2	12.7	0.1		

Figure 9C

Clone
Design
R20-4-C10-IGFR

Sequence
XXXXXXXXXXXXXXXXXXXX
PKGTRFRGDDVDVWDGYSLA

Ratios over Background			Comparisons	
E-Tag	IGFSR	IR	IGFR/IR	IR/IGFR
--	--	--	--	--
37.8	3.8	--	--	--

Figure 10A

Clone	Sequence	Ratios over Background				Comparisons	
Design	XXXXXXXXXXXXXXXXXXXX	E-Tag	IGF _R	IR	IGF/IR	IR/IGF _R	--
20F-4-B7-IGFR	TPIPAGGINIASWGGYTWLS	10.9	3.7	0.5	7.3	0.1	
20F-4-E4-IGFR	HRGTVTGVWVARWPGYEMLS	8.9	4.7	0.7	6.3	0.2	
20F-4-E12-IGFR	SDVWAQOPQRRNDWPGYHMLS	9.7	4.7	0.8	6.0	0.2	
20F-4-F4-IGFR	HRGTVTGVWVARWPGYEMLS	13.9	10.1	1.8	5.6	0.2	
20F-4-F7-IGFR	SDVWAQOPQRRNDWPGYHMLS	13.7	3.9	0.8	5.1	0.2	
20F-4-E7-IGFR	RPHRINPQDDAVWPGYLMG	7.2	2.5	0.5	4.7	0.2	
20F-4-F11-IGFR	HRGTVTGVWVARWPGYEMLS	17.6	16.2	3.5	4.6	0.2	
20F-4-D10-IGFR	FGRGYGGDGGGYWSGYEWLA	9.8	2.4	0.6	4.1	0.2	
20F-4-B3-IGFR	DGLVVKSGREMPGYMLER.A	17.3	14.4	3.6	4.0	0.2	
20F-4-B12-IGFR	DGSIV.VSSSVGMPGYEMLM	10.1	9.9	2.4	4.0	0.2	
20F-3-A9-IGFR	WQQANLSNGCGRWGYDMLM	6.6	2.7	0.7	4.0	0.2	
20F-4-G2-IGFR	FGRGYGGDGGGYWSGYEWLA	5.1	1.3	0.5	2.7	0.4	
20F-4-D11-IGFR	VNYEMDRVPEMPMGYWMLS	5.0	1.0	0.5	2.3	0.4	
20F-4-G4-IGFR	MGGGLWGVH1WPGYSWLSQ	3.9	0.9	0.5	1.8	0.6	
20F-4-G12-IGFR	SDVWAQOPQRRNDWPGYHMLS	3.2	0.9	0.6	1.5	0.7	

Figure 10A (Con't)

Clone	Sequence	Ratios over Background				Comparisons	
Design		E-Tag	IGfSR	IR		IGfR/IR	IR/IGfR
R20β-4-A4-IR	XXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	--
R20β-4-F2-IR	WPGYLFEEALQDWRGSTED	11.9	17.5	1.4	12.5	0.1	0.1
R20β-4-E8-IR	SMFVAGSDRMPGYGLADWL	16.4	13.9	3.1	4.5	0.2	0.2
	VRGFGGTVMWPGYEWLRNAA	41.0	34.9	3.6	9.7	0.1	0.1

Figure 10B

Clone
Design
20F-4-H10-IR
20F-4-C10-IR

Sequence
XXXXXXXXXXXXXXXXXXXX
LDLASGDSWLGVDVLRGWL
IHSSDGI GAWGYA WFRDVA

Ratios over Background			Comparisons	
E-Tag	IGFR	IR	IGFR/IR	IR/IGFR
--	--	--	--	--
10.2	3.1	2.4	1.3	0.8
23.4	9.6	4.1	2.3	0.4

Figure 10B (Con't)

Clone Design	Sequence	Ratios over Background				Comparisons	
		E-Tag	IGF ₁ R	IR	IGF ₁ R/IR	IR/IGF ₁ R	
	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	
R20f-4-p10-IR	LGPLLRWGSEVCGVWPDLCE	21.5	1.0	8.0	0.1	8.0	
R20f-4-p9b-IR	PFQFGGRWGI PRMWWYRNS	32.6	6.8	15.1	0.5	2.2	
R20f-4-H4-IR	MMWGGRNRMWLERWGLGGER	11.6	1.7	3.6	0.5	2.1	
R20f-4-A2-IR	GRVALWGPVWPRWWMFSRPV	17.1	2.6	5.2	0.5	2.0	

Figure 10C

Clone Design	Sequence
R20-4-F10-IGFR	XXXXXXXXXXXXXXXXXXXX
R20-4-F7-IGFR	CLGAGSFRAGILCLGGLPVS
R20-4-H9-IGFR	GFWATACGGLQICEELGLKP
R20-3-A4-IGFR	DLFCAYMAQALGLGQDLSCG
	RHLLLPQIWIAS*GGWGMG

Ratios over Background			Comparisons	
E-Tag	IGFsr	IR	IGFR/IR	IR/IGFR
--	--	--	--	--
35.5	6.0	--	--	--
29.1	4.7	--	--	--
25.7	3.0	--	--	--
15.6	2.7	--	--	--

Figure 10E

Clone	Sequence	Ratios over Background				Comparisons	
Design	Sequence	E-Tag	ICFsR	IR	ICF/IR	IR/ICF	IR/ICF
20C-3-H3-IGFR	XXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	--
20C-3-F4-IGFR	PHRLCGTDEYLMQDLFVRGLCRLIM	28.5	26.6	1.0	26.6	<0.1	<0.1
20C-4-C10-IGFR	GLLFCKQLFTLAGLQPEAGCVSSSR	34.4	27.5	1.2	23.1	<0.1	<0.1
20C-3-G5-IGFR	IWIACLDLRLRGQVWSSCRRAPIG	35.5	24.4	1.3	19.2	0.1	0.1
20C-3-A2-IGFR	DWLRLGVILSGGLTELANTGCVQG	29.3	21.1	1.1	18.7	0.1	0.1
20C-3-B4-IGFR	WFSFCLGGLQAQEMSVWGRDVGCI	33.9	18.3	1.1	16.9	0.1	0.1
20C-3-C6-IGFR	GYSWLRDVLMEKQAKREGSVGRQ	39.8	29.1	1.9	15.2	0.1	0.1
20C-3-E2-IGFR	FLTRLRLGLS*ERGEAGGPYAQA	34.8	20.9	1.4	14.9	0.1	0.1
20C-3-A3-IGFR	FSGFCMGLERLSQVSLGYCGAGQGG	34.8	28.1	2.0	14.2	0.1	0.1
20C-3-B1-IGFR	ISFRCLFVLGMPDPCPDVGGEGF	33.7	14.3	1.2	12.4	0.1	0.1
20C-3-F5-IGFR	NTPNCSQDWGQESGFMAALLLATCK	30.2	9.8	0.9	11.2	0.1	0.1
20C-4-A7-IGFR	LQGFCELLATVTGVTGLGCLDYQPI	35.5	31.9	3.9	8.2	0.1	0.1
20C-4-F8-IGFR	GSSICNLARAQIVELALCEMVGQE	33.3	19.3	2.8	6.9	0.2	0.2
20C-4-G11-IGFR	LSFACLLSQLSGVLPDCLLGED	30.5	27.7	5.3	5.2	0.2	0.2
20C-3-E1-IGFR	GEHFCQLMSLCGDDCGPVNCGGGS	24.7	13.3	2.8	4.7	0.3	0.3
20C-3-B6-IGFR	GMFECLLASLVLGVPQGRSRASAVC	34.0	5.1	1.6	3.1	0.3	0.3
	YRQECACSVGAVGFLCGLACLARSG	37.3	32.8	13.7	2.4	0.4	0.4

Figure 10F

Clone	Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGF ₃ R	IR	IGF ₃ R/IR	IR/IGF ₃ R
		XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
	40F-4-D1-IGFR	LSCLAYSRHGIMWRPSTDGLGRSVGEGSVSTRMRGYDWF	4.9	4.6	0.3	13.1	0.1
	40F-4-B1-IGFR	GLDHSDAVGVHLGFAMPA.ARGKWEAGGLEDTWAGYDWL	4.1	3.0	0.2	13.1	0.1
	40F-4-D10-IGFR	W.GYAWLS	4.9	4.5	0.4	11.7	0.1
	40F-3-A3-IGFR	LSCLAYSRHGIMWRPSTDGLGRSVGEGSVSTRMRGYDWF	2.6	2.0	0.3	7.9	0.1
	40F-4-C4-IGFR	EAMAVGLQCPRFVRRAAAHGDGSGMGQDHV.AWGGYMWLG	3.8	2.0	0.5	4.1	0.2

Figure 10F (Con't)

Clone	Parental/Design	Sequence	Ratios over Background				Comparisons	
			E-Tag	IGF1R	IR	IGF1R/IR	IR/IGF1R	
		HLGVLEELFMGASLFGYCSG	39.1	1.8	27.7	0.1	15.4	
	F815-4-G11-IGFR	HFYVLVERLSGASLFGSGSA	34.6	7.9	1.0	7.9	0.1	
	F815-3-D1-IGFR	HRFVREGLLMGAYQFCYCSCG	14.9	1.0	2.0	0.5	2.0	
	F815-4-C12-IGFR	FQSLLEELVMGAPLFRYCTG	35.2	1.0	2.0	0.5	2.0	
	F815-4-A11-IGFR	HLSVLEELSWGASLFGQWAG	5.4	1.0	2.1	0.5	2.1	

Figure 10G

Clone	Parental/Design	Sequence	Ratios over Background					Comparisons	
			F-Tag	IGF ₁ IR	IR	IGF ₁ IR/IR	IR/IGF ₁ IR	IR/IGF ₁ IR	IR/IGF ₁ IR
	NNKH-4-A9-IR	HLSTLEELSMGASLFGQWAG	5.4	1.0	2.1	0.5	2.1	2.1	2.1
	NNKH-4-H4-IR	NLCRLLEELAMGASLFGQACAG	16.3	1.0	2.7	0.4	2.6	2.6	2.6
	NNKH-4-B3-IR	APVSTEEELRWGALLFGQWAG	15.6	1.0	2.6	0.4	2.5	2.5	2.5
	NNKH-4-E1-IR	HLSTLEERWMMRESLFGQWAG	13.6	2.8	6.7	0.4	2.3	2.3	2.3
	NNKH-4-E7-IR	HLSTLEERWMMRAALFGQWAG	13.9	4.8	9.5	0.5	2.0	2.0	2.0
	NNKH-4-C3-IR	HLSTLEEQWMMRESLFGQWAG	16.9	1.3	2.3	0.6	1.8	1.8	1.8
	NNKH-4-B6-IR	HMSVEELSMWASLFGKOAG	11.3	1.3	2.3	0.6	1.7	1.7	1.7
	NNKH-4-A10-IR	HLSELEERWMMRATLFGQWAG	13.2	1.3	2.1	0.6	1.7	1.7	1.7
	NNKH-4-A5-IR	HLSTLEELWMMRESLFGQWAG	15.4	2.0	3.2	0.6	1.6	1.6	1.6
	NNKH-4-F11-IR	HLSTLEEQWMMRESLFGQWAG	14.6	4.6	6.9	0.7	1.5	1.5	1.5
	NNKH-4-C9-IR	HLSTLEERWMMRATLFGQWAG	14.0	3.1	3.9	0.8	1.3	1.3	1.3
	NNKH-4-D12-IR	HLSTLEEQWMMRESLFGQWAG	14.3	2.3	2.9	0.8	1.3	1.3	1.3
	NNKH-4-D10-IR	HLSTLEEQWMMRESLFGQWAG	12.0	1.4	1.7	0.8	1.2	1.2	1.2
	NNKH-4-E5-IR	HLSTLEELWMMREALFGQWAG	13.6	1.2	1.5	0.8	1.2	1.2	1.2
	NNKH-2-A6-IR	HLSTLEERWMMRATLFGQWAG	14.5	1.4	1.6	0.9	1.1	1.1	1.1
	NNKH-4-F6-IR	HLSTLEELWMMRATLFGQWAG	8.4	1.4	1.5	1.0	1.1	1.1	1.1
	NNKH-4-C7-IR	HLSTLEEQWMMRATLFGQWAG	14.1	2.8	2.9	1.0	1.0	1.0	1.0
	NNKH-4-F7-IR	HLSTLEERWMMRATLFGQWAG	14.7	1.4	1.4	1.0	1.0	1.0	1.0
	NNKH-4-F8-IR	HLSTLEELWMMRESLFGQWAG	14.1	7.5	7.0	1.1	0.9	0.9	0.9
	NNKH-4-E9-IR	HLSTLEEQWMMRESLFGQWAG	13.6	11.0	8.6	1.3	0.8	0.8	0.8
	NNKH-4-E6-IR	HMSVEELWMMRATLFGQWAG	15.5	7.9	6.0	1.3	0.8	0.8	0.8
	NNKH-4-B7-IR	HLSTLEERWMMRATLFGQWAG	18.2	3.8	2.7	1.4	0.7	0.7	0.7
	NNKH-2-B3-IR	HRSVLKQLSMGASLFGQWAG	16.5	12.9	8.2	1.7	0.6	0.6	0.6
			11.5	5.3	0.7	7.4	0.1	0.1	0.1

Figure 10H

Clone	Parental/Design	Sequence	Ratios over Background					Comparisons	
			ε-Tag	IGF:R	IR	IGF:IR	IR/IGF:R	IR/IGF:R	IR/IGF:R
		HL*VLEEL*SWGASLFGQWAG	5.4	1.0	2.1	0.5	2.1	0.8	2.1
NNKH-2-C5-IGFR		HL*VLEEL*SWGASLFGQWAV	7.3	0.9	0.7	1.3	0.8	0.8	0.8
NNKH-2-D9-IGFR		HL*VLEEL*LGASMFGLWAG	4.1	0.5	0.4	1.3	0.8	0.8	0.8
NNKH-2-H12-IGFR		HL*SVLKE*SWGASLFGQWAG	5.0	1.3	1.1	1.2	0.8	0.8	0.8
NNKH-2-D10-IGFR		HL*SVLEEL*SWGASLFGQWAG	4.8	2.1	1.9	1.1	0.9	0.9	0.9
NNKH-2-G9-IGFR		HL*SVLAEL*SWGASLFGQWAG	1.9	1.4	1.3	1.1	0.9	0.9	0.9
NNKH-2-C6-IGFR		RL*SVLEEL*SWGASLFGQWAG	18.2	1.0	0.9	1.1	0.9	0.9	0.9
NNKH-2-C7-IGFR		HL*VLVOP*SWGASLFGQWAG	21.8	1.3	1.3	1.0	1.0	1.0	1.0
NNKH-2-F11-IGFR		HOSVLEEL*SWGASLFGQWAG	6.7	1.3	1.4	0.9	1.1	1.1	1.1
NNKH-2-H3-IGFR		DMSVLEEL*SWGASLFGQWAG	4.7	0.7	0.8	0.9	1.1	1.1	1.1
NNKH-2-B8-IGFR		HL*SVREGQ*SWGASLFGQWAG	17.5	3.7	5.2	0.7	1.4	1.4	1.4
NNKH-2-B12-IGFR		QL*SVLEEL*SWGASLFGQWAA	1.2	1.0	2.9	0.3	2.9	2.9	2.9
NNKH-2-F9-IGFR		HL*SVGEEL*SWGASLFGQWAR	3.7	0.6	2.1	0.3	3.5	3.5	3.5

Figure 101



D Name	Clonal Name	Formula #	K _d (μM) HIR	P.O.	Fat Cell Assay	Activity	K _d (μM) HIR	Ratio IGF/IR	Sequence
D101	20D3	1	0.51 0.27				13 11	23 41	KIGGQQQIHIQDGNFYDWFVEALAKK (ε-biotin)
D102	20D1	1	1.2 0.97				7.4 16	6.2 16	KVLQARHIGCDVSDCFYEFWFAKK (ε-biotin)
D103	H8	1	0.74				15 16	20	KWSALSYMDTGFYAWFDDAVKK (ε-biotin)
D104	E7	1	20				>20	>1	KGLISVALVRIVDRIFYEFWFDLKK (ε-biotin)
D105	H8	1	2.8				12	4.3	KRDQPTDQEEQNVSFYEFWRJLKK (ε-biotin)
D106	20F1	1	0.97				6.2	6.4	KVFVNCRSQQLDFYEFWFEQAQKK (ε-biotin)
D107	40G11	1	1.1	YES		Antagonist	9.7	8.8	KLESIIYVPOALDRLFYSWESKK (ε-biotin)
D108	3G1T	1	2.3			Antagonist	19	8.3	KFYGWESROLSTPRDDWGLPKK (ε-biotin)
D109	20H1	1	3.6			Antagonist	12	3.3	KSAHGLVSNKQDGLFYSWFREKK (ε-biotin)
D110	G3	1	0.84			Antagonist	1.4	1.7	KRGGGTIFYEFWESALRKIGAGKK (ε-biotin)
D111	D2	1	0.62			Antagonist	3.2	5.2	KDIERMQSDVGFYEFWRFAVGKK (ε-biotin)
D112	IGFR C1 A65-4-C1	1	0.49 0.19			Neutral	0.05* 0.02*	0.1 0.1	DYKDCWARPCGDAAAFYDWFVQQAASKK (ε-biotin)
D113	IGFR I12 A65-4-1+2	1	0.75		-20 μM	Agonist	5.4	7.2	DYKDVFTSAVFIEIFYDWFVRQVSKK (ε-biotin)
D114	IGFR A6	1	8.1			Neutral	>20	>2.5	SAKNFYDWFVKK (ε-biotin)
D115	IGFR D5	1	8.1				>20	>2.5	ADKNFYDWFMAAKK (ε-biotin)
D116	IGFR JBA5	9	4.4 cycl		>20 μM	Agonist	8.1	1.8	DYKDCOSWGWIRIGWLAGLCPKK (ε-biotin)
D117	IGFR I12C	1	0.70	YES	-20 μM	Agonist	6.1	8.6	FIENFYDWFVRQVSKK (ε-biotin)
D118	20E2	2	0.25	YES	-20 μM	Agonist	1.3	5.2	DYKDFYDAIDQLVRGSARAGGTRDKK (ε-biotin)
D119	20C11	2	0.25	YES	-20 μM	Agonist	13	2.9	KDRAFYNGLRDLVGA VYGAWDQKK (ε-biotin)
D120	E8	10	0.37			Antagonist	2.2	5.9	KVRGFGGCTVWPGEWLRNAKK (ε-biotin)
D121	F2	10	1.1			Antagonist	7.4	6.7	KSMFVAGSDRWPGYGLADWLKK (ε-biotin)
D122	20A4 (A7)	6	1.2 1.0			Antagonist	>20	>17 >20	KEIEAEWGRVRCLVYGRCVGQKK (ε-biotin)
D123	D8	6	0.55 1.3			Antagonist	16 >20	29 >15	KWLDQEWAWVQCEVYGRGCPSSKK (ε-biotin)
D124	F8	4	0.04* 0.09*				8.2 >20	200 >200	KIILCVLEELFWGASLFGYCSGKK (ε-biotin)
D125	IGFR E4	1	2.6				>20	>8	DYKDESAAGFRGNFYDWFVAQVNAKK (ε-biotin)
D126	IGFR D2C	1	1.4				18	13	LGENFYDWFVMAQVRKK

Figure 11A



Clonal Name	D or S name	Munit	Sequence	IR-Kd	IR-IC ₅₀ Biacore	IR-IC ₅₀ FP-S175	PO ₂	Fat Cell Assay
20-E2	D118	Ib6	DYKIDFYDAIDQLVRGSARAGGTRDK-K-biotin	250 nM		2.8 nM	+	++
C1	D112	A6	DYKIDWARPCGDAANFYDWFVQOAS-KK-biotin	490 nM			-	0
D8	D123	C-C10XP	KWIDQEWAWVOCEVYGRGCSKK	550 nM			0	-
E8	D120	G10UP 6	KRGQCGIWWPGYEWELRNA	370 nM			-	-
F8	D124	C-C10XP	KHLCVLEELFWGASLEFGYCSGKK	40 nM			-	0
I12C	D117	A6	FIHINFYDWFVWQVYSKK	700 nM			++	++
KCF9			RIYYIEWWQGLEAGRGGLS			5 nM		
KC-G2		C-C-C	GHEQCGWVGLEVOGRGCS					
KCG7		Ib6	FYCGLEELSWGALFGYCSG					
NG-C2		Ib6	GNGIXGMFYQLSLVGDMH		<1 µM			
NG-G33		A6	GISQSCRESYDWFAGQVSDPWWCW		2-4 µM	4.2 nM	+++	
NG-G8		B6	VEGIGLFYDLRQLARRONG		>5 µM		-	
NG-G9		B6	RAMSEYDAI VSVLGLGPKK-Biotin				-	
RP-1		A6	OSNVFHEQFYEWFDQLGL		1 µM		+	
RP-2		A6	RSEAFHVEFVSWFEQLRS		1 µM		+	
RP-3		A6	GRFYGWFDQIDQLMPWGFID		>10 µM		-	
RP-4		B6	PPWGAIFYDAIEQLVFDNI		5 µM		+	
RP-5		B6	AGVNAGFYHVESLIDWWDQGGK-Biotin		6 µM		-	
RP-6		Ib6 + C-C	TFYSCLASLLIGTPQPNRGPWERCRRK-Biotin				+++++	
RP-7		A6	AAVHIEQFYDWFADQYKK					
RP-8		B6	QSFYDYIEELLGGEWKK		>5 µM		+	
RP-8#	S287	Ib6	QSFYDYIEELLGGEWEE					
RP-9		A6	GSLIDSEFYDWFERQLGKK			2.9 nM	++	
RP-10		B6	GSEFYALQRLVGGEQGGK		>10 µM		+	
RP-11		A6	OAPSNFYDWFVREWDKK		>10 µM		+	
RP-12		B6	DPEYQGLWEWLRESGKK					
RP-13		A6	ASGFEINFYDWFGRQLSLKK		>10 µM			
RP-14		A6	SACQIDCHENFYDWFAROKK		>10 µM			
RP-15		A6	SOAGSAFYAWFDQVLRVKK					
RP-16		B6	V.DARDIDFULSEVTL					
RP-17		B6	QSDAIFYSGLWALIGLSDGKK		>10 µM			
RP-18		B6	LQPCSGFYECIERLIGYKK					
RP-19		A6	LKDGFYDYFWORHLGSKK					
RP-20		B6	GSASFYDAIDRLRMRIKK					
RP-24		GROUP 6	WPGYLFEEALQDWROSTED					
S167	S167	A6	AFYDWFVAKK	>20 µM	No Binding		-	
S173	S173	RB6	LDALIDRLMRYFEERPSL	1.2 µM				
S174	S174	RIb6	PLAELWAYFEIISEOGRSSAI	16 µM				0
S175	S175	A6	GRVIDWLQRNANFYDWFVAELG	230 nM	2-4 µM	0.9 nM	++	0
S176	S176	A6	NGVEAGTGDNIFYDWFVAQLI	470 nM				+++

Figure 11B



Clonal Name	D or S. name	Molt	Sequence	IR-Kd	IR-IC ₅₀ Diacore	IR-IC ₅₀ FP-S175	RO ₁	Fat Cell Assay
S177	S177	H6	EIWNIVDPFYFTLFEWLRESG	2.7 μ M				+
S178	S178	H6	EIWNIVDPFYQYSELRESG	130 nM				0
S179	S179	A6	QSDSGIVIDHFGWFRDIWAS	540 nM				++
F8-C12	S224	C-C100P	FQSLLEH.VMGAPLFRYGIG					
S225	S225	C-C100P	PLCVLEELFWGASLFGYCSG					
H8-G1	S226	C-C100P	QLEEWAGVOCEVVGRCPS					
S264	S264	A6	IQWIEPFYGWFDVVAQMTEE					
S257	S257	H6	RWINEYGYFESLTHIFS					
S258	S258	H6	HYNAFYEFQVLLAETW					
S259	S259	H6	EQWDFYSTSGLLASVT					

Figure 11B (Con't)

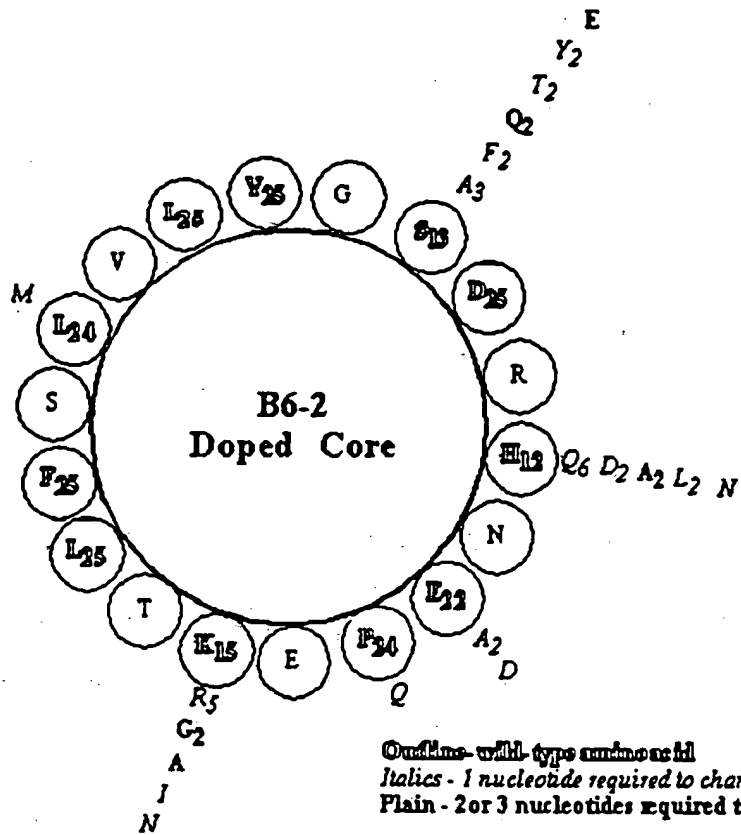


FIGURE 12

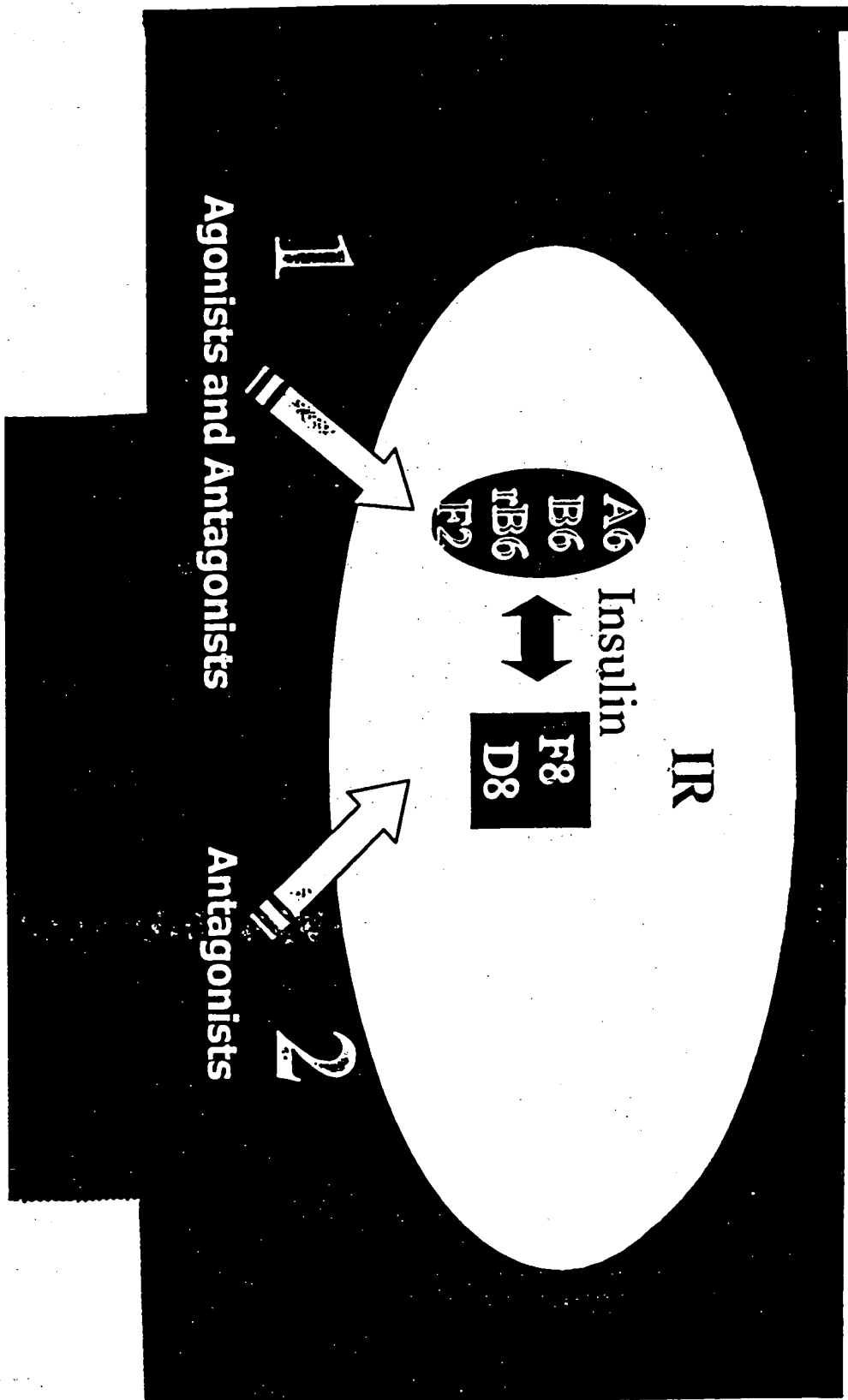


FIGURE 13

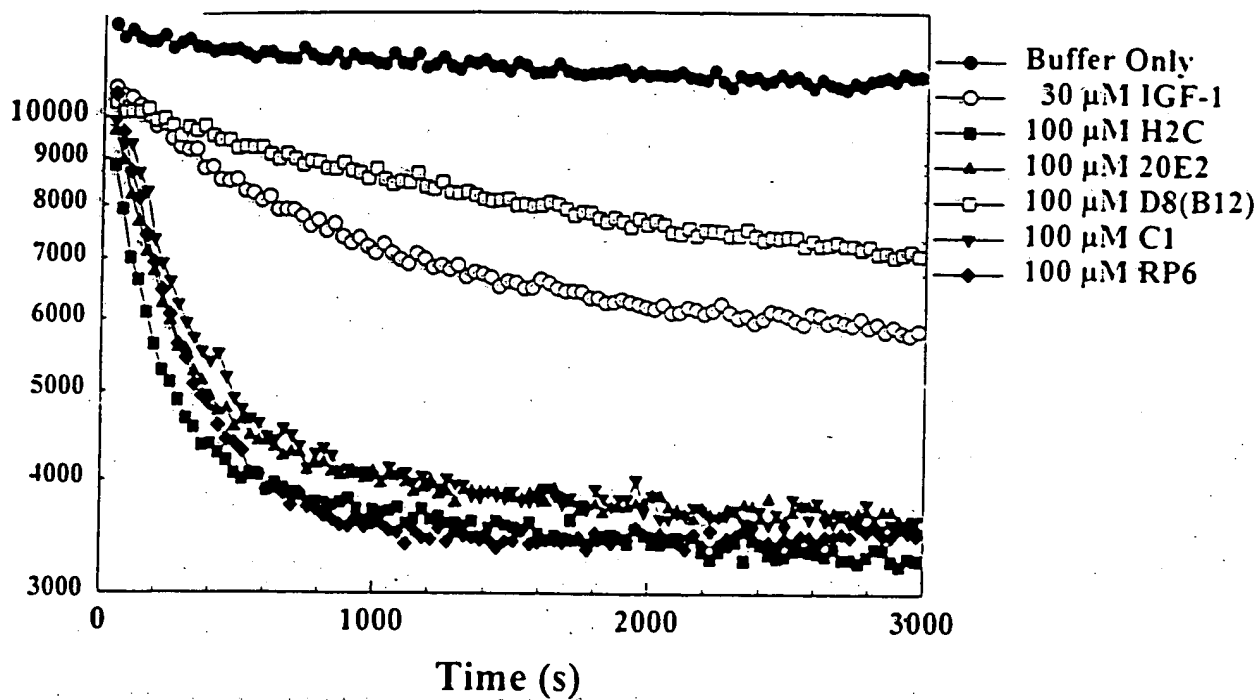
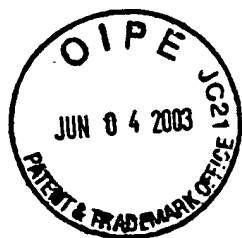


FIGURE 14

Intra-receptor Binding

Inter-receptor Binding

Site 1
 Site 2

Di-Peptides
 Binding to IR
 replaces Insulin

OR



FIGURE 15

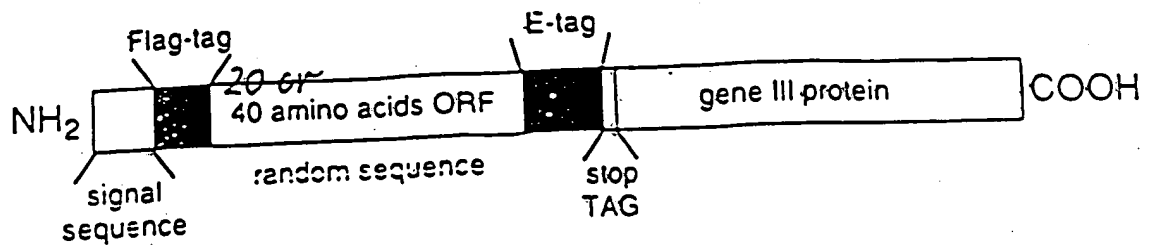


FIGURE 16

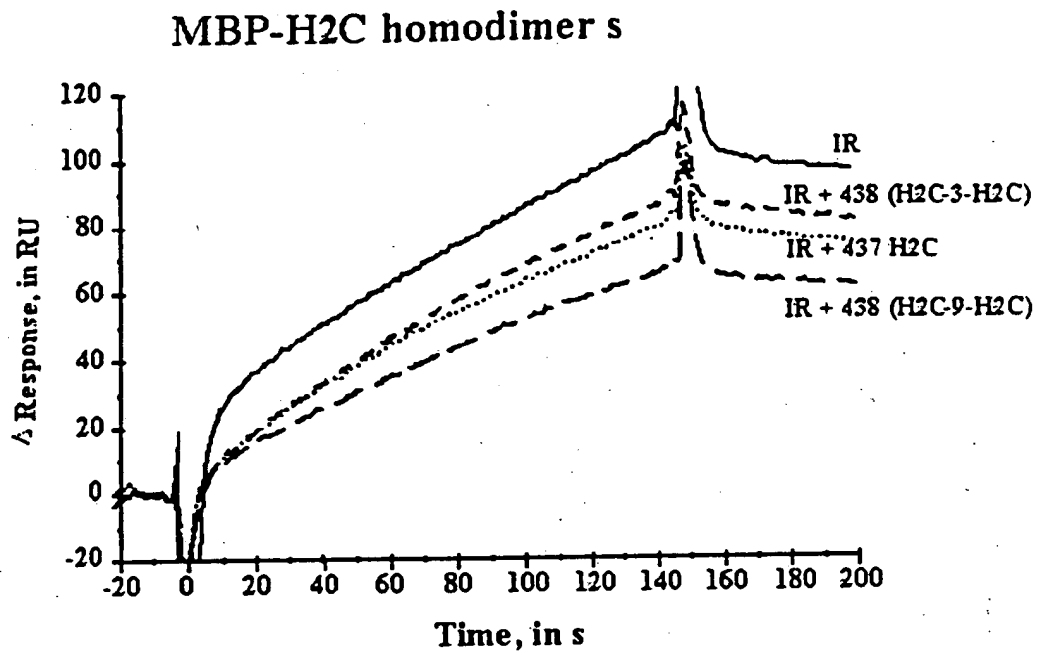


FIGURE 17



Class I clones

		# Clones:				Competition
		Rnd 3	Rnd 4			
B6 3x	DYKDAETPAQVGWNR ¹ LSVWPGEH ² WNTVDPEYH ³ KLSEL ⁴ RESGA	1	2			+
E5 2x	DYKDRHLTNAELGVSP ¹ EVL ² SLRLEP ³ DDIEFYRA ⁴ LSHLV ⁵ RGMGPP	2				+
B5 2x	DYKDRGMDRQWL ¹ DVGARI ² RLERSV ³ QDNTDPEYGL ⁴ RLVDGF	2				nd
9	DYKDCRPDSFDVTEKGD ¹ MAILNVR ² FDPHSL ³ DENDQTEYEL ⁴ LD ⁵ SL			1		nd
G6	DYKDGTYFERGQVAQ ¹ SNE ² SLRVN ³ ELQ ⁴ LE ⁵ LAASPT			1		nd
12	DYKDAPLDARLSAP ¹ RQWSP ² RTWRQ ³ SLSYGEW ⁴ SCSEFYD ⁵ CLSSI			1		nd
A5	DYKDMGSSQFQDTRP ¹ SSGQAYSH ² SLSDG ³ WTANW ⁴ IFLRA ⁵ LEGL			1		nd
C6	DYKDSGAALIEGNQ ¹ GRE ² RSTHLA ³ ANIND ⁴ HLPGDAG ⁵ IWLGY ⁶ SWLS			1		+
Consensus (regular+frameshifters)		d.fy. llsal				

human IGF mature

VCGDRGEYFNKPTGYGSSSR

human IGF propeptide

MSSSHLEFLALCLLTFTSSA

-16 -9

Class I frameshifting clones (all in +1 frame)

F6 2x	TTKTRG.IFGMLGLVLR ¹ FQILLW ² FPKDCV ³ QMKDIE ⁴ YSLSL ⁵ SL	1	1		+
7 3x	TTKTRIGCCS.LVWGWRGCR ¹ LADGE ² YAFIM ³ ALA ⁴ AG		3		nd
8	TTKTRLRL ¹ LLLLGGE ² PEFYGL ³ RLMLIG ⁴ RGS		1		nd
G5	TTKTGWFAWV.LAFSVQGV ¹ VAFYSA ² LAALLCA ³ HSASL ⁴ VCGA	1			nd

Class II clones

D5	DYKDPLYGGGIHL ¹ YPGTMG ² YVPGEP ³ RQVK ⁴ VLGDAD ⁵ KNFYD ⁶ WEM	1			nd
A6	DYKDYRGMLVL ¹ GRISD ² GAGK ³ VASEP ⁴ PARIG ⁵ QKVFA ⁶ VNEYD ⁷ WEV	1			nd
R35	DYKDSGCCRL ¹ LGLRM ² FIVIVG ³ SGALVC ⁴ QSAASA ⁵ AGFYD ⁶ WEV	1			

human IGF mature (1-70)

GPETLGAEL VDALQFVCGD RGEYFNKPTG YGSSSRAPQ TGI¹VECCFR SC²DLRL³LEMY CA⁴PLKPAKSA

nd = no data

FIGURE 18



IGF-5
GACTACAAAG ACCGAGTTC GAGTTCCTI TACGTCCTC GAGGCTTCA GCTTTCAGI TCTTCCTCC GCGTTTCTA AGGATTCIGI TCAATCAAA GATATTTI AATCTTCIT GAGTTCCTC GCGGCTTCA 139
D Y K Q S M I M F R Y V A G R A Q V S D S S V A V S . G L C S D E R Y F L F V V G Q F G G R
I T K T R G . I F G M L L G V L R I Q I L L M P F P K D C V Q M K D I F Y S L L A S L A A A
L Q R L V V I F S V C C M A C L G F R I F C G R F L R I V I R . K I F F I R C M L V M R P

IGF-6
GACTACAAAG ACCGAGTTC GAGTTCCTI TACGTCCTC GAGTTCAGC CTTCATTC GCTTCCTCCTI ATCTTCATTC GCTTCCTCCTI TCGGCTTCA 180
D Y K Q A V A A A V A P M G . A F L N A S P Y A D M S M V C G R
I T K T R L R I L L I L G G D E P F Y G L L R M L I G R G S A A A
L Q R R G C G C C C S L G V M S L F M G F S V C . L V V G L R P

IGF-05
GACTACAAAG ACCGAGTTC GAGTTCCTI TACGTCCTC GAGTTCAGC CTTCATTC GCTTCCTCCTI ATCTTCATTC GCTTCCTCCTI TCGGCTTCA 139
D Y K Q M L V C L G V M I S F F C L G G R C G F L L S V G C L V V C P Q C F F G V M C G G R
I T K T R G M F A M V . I A F S V Q G V G V A F Y S A L A A L L C A H S A S L V C G A A A A
L Q R L V G L L G C D D Q L F L F R G S V M L F T Q R M L P C C V P I V L L M C V V R R P

IGF-7
GACTACAAAG ACCGAGTTC GAGTTCCTI TACGTCCTC GAGTTCAGC CTTCATTC GCTTCCTCCTI ATCTTCATTC GCTTCCTCCTI TCGGCTTCA 112
D Y K Q P D M V L Q L I S L G L E G M Q I G . M V L C V I D G A G M G G R
I T K T R I G C C S . L V M G M R G C R L A D G F Y A F L M A L A G A A A
L Q R P G L G V V A D Q F G V G G D V D M L M G I M R I . M R M L G R P

FIGURE 19

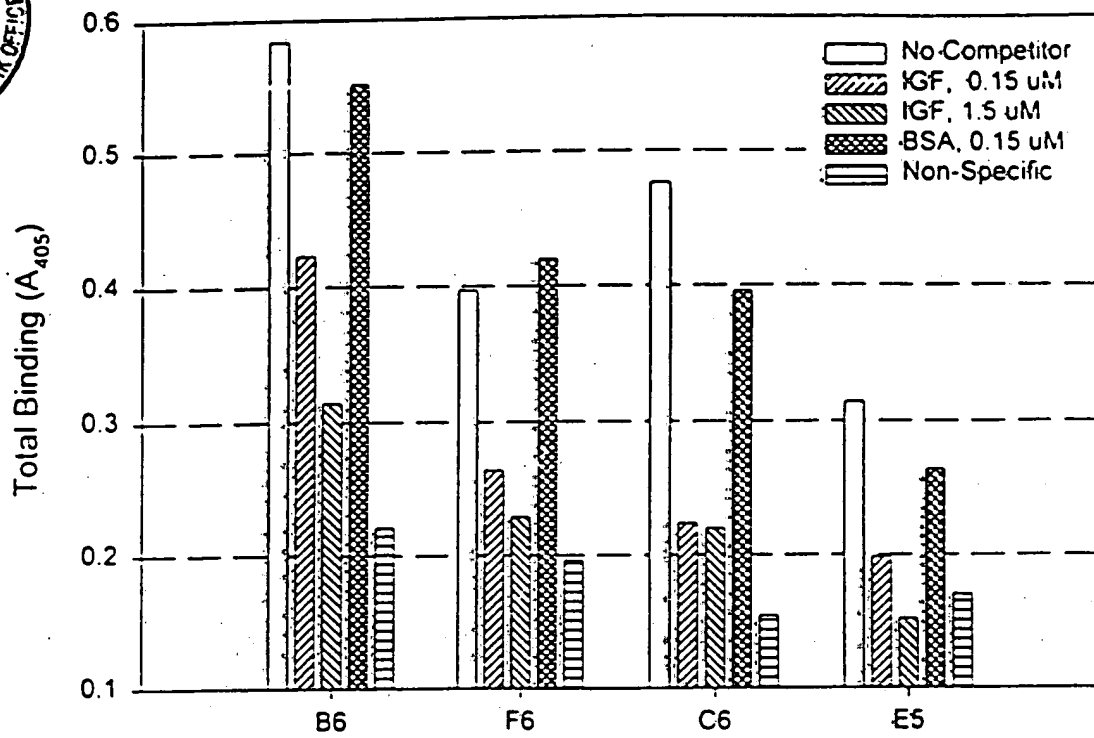


FIGURE 20A

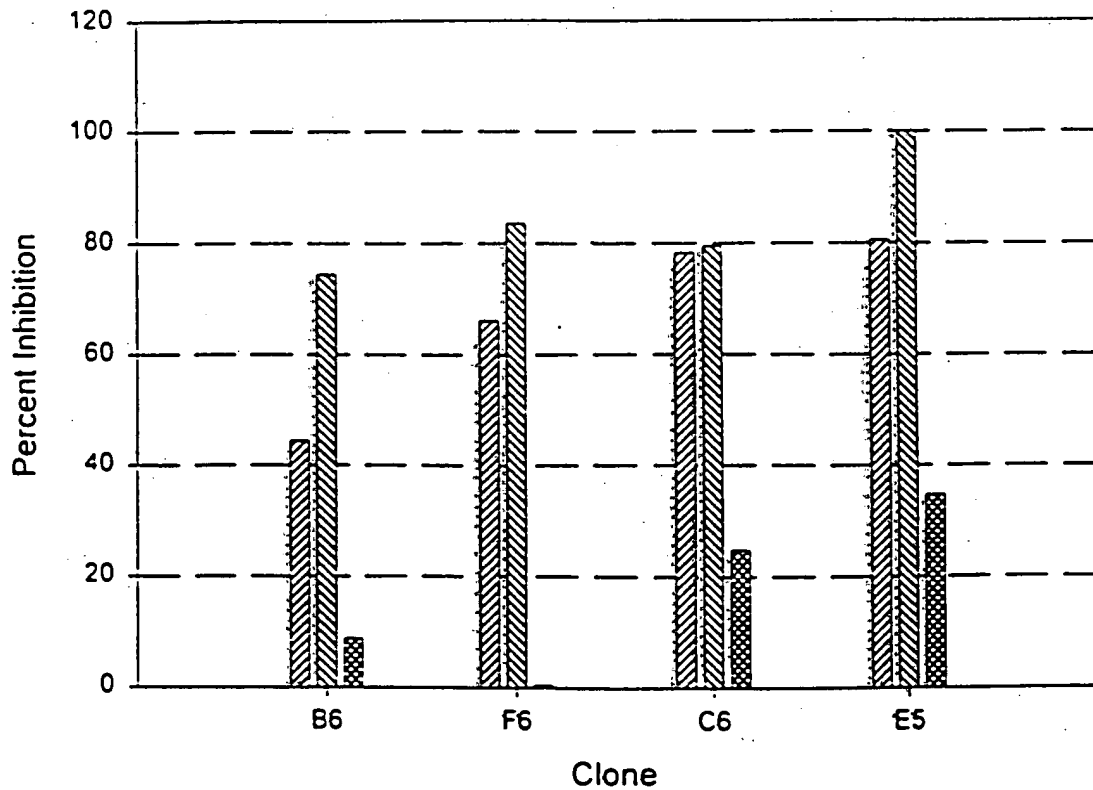


FIGURE 20B

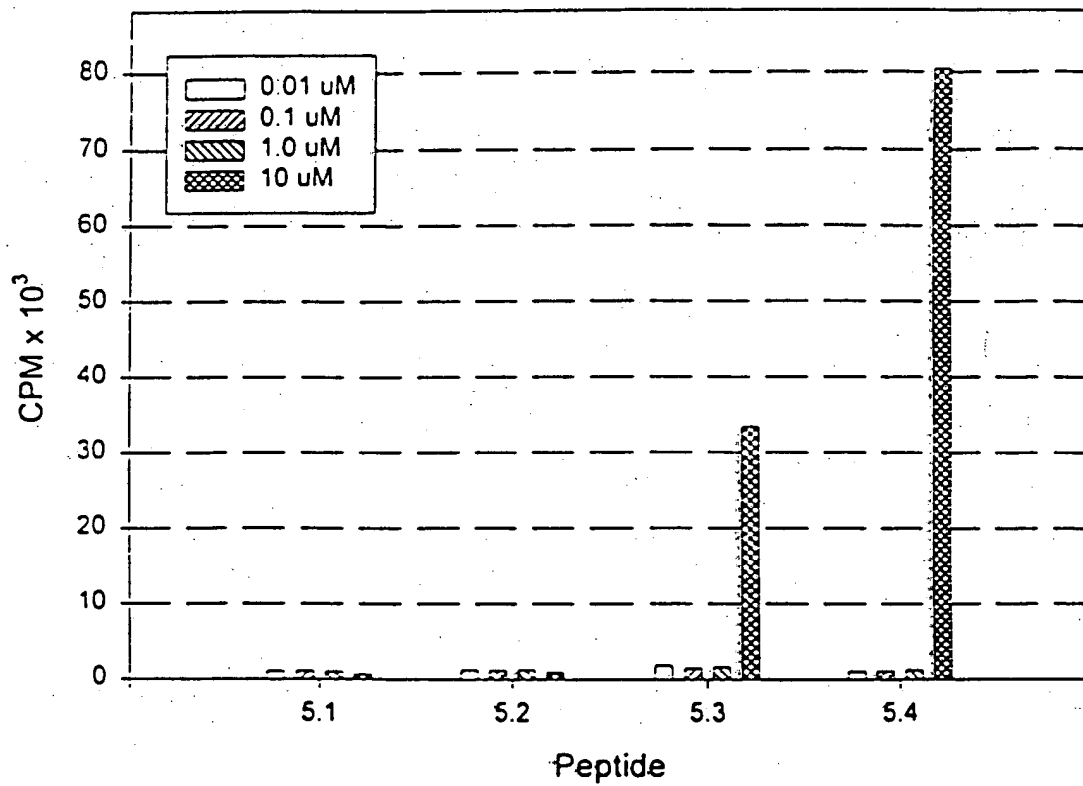


FIGURE 23

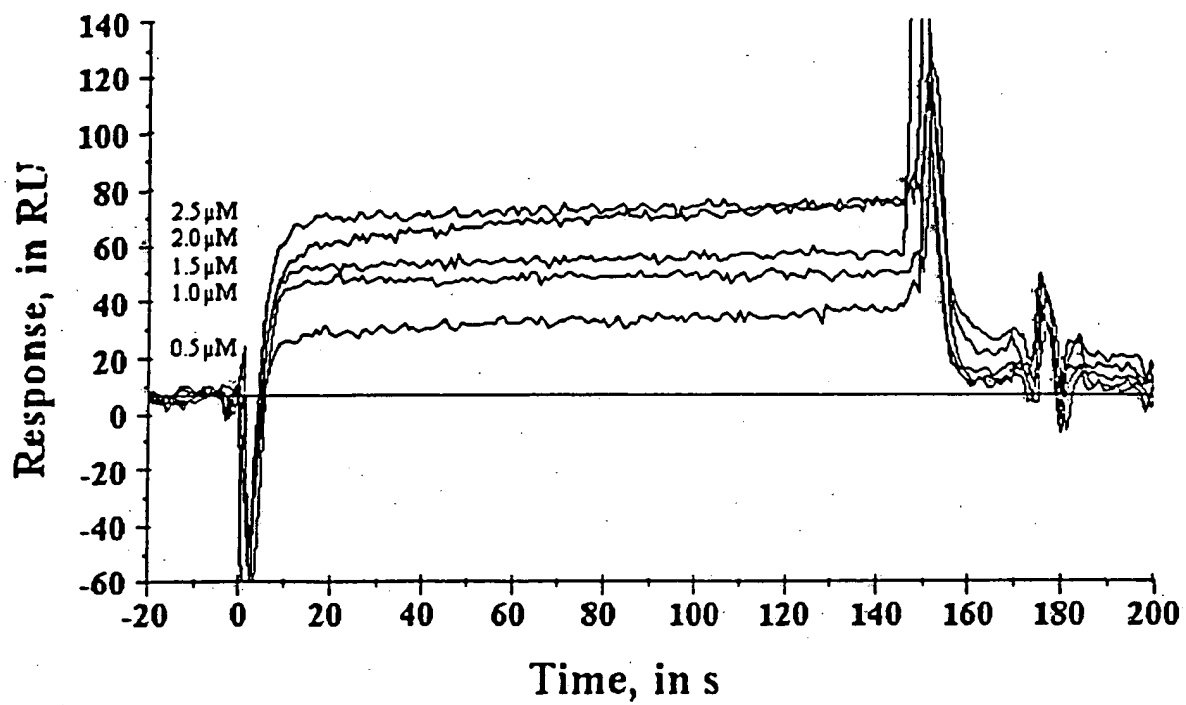


FIGURE 24A

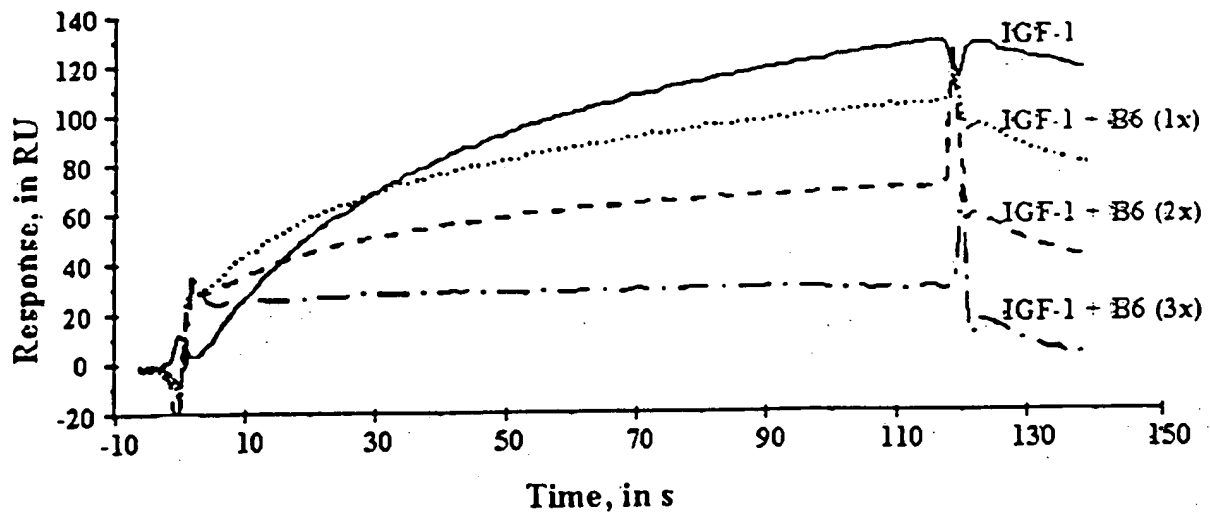


FIGURE 24B



GACTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGTTCTGGGTCGTATCTCTGACG
D Y K D D D D K Y R G M L V L G R I S D

GTGCTGGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCCGCTGTTAA

G A G K V A S E P P A R I G Q K V F A V N

CTTCTACGACTGGTTTCGTTGCGGCCGCA 96 nt
F Y D W F V A A A

FIGURE 25A

CTACAAAGACGACGATGACAAGTACCGTGGTATGCTGGTTCTGGGTCGTATCTCTGACGGTGCT
GGTAAAGTTGCTTCTGAACCGCCGGCTCGTATCGGTCAGAAAGTTTTCGCTGTTAACTTCTACG
ACTGGTTTCGTTGCGGCCGCGAGTGTGA 154 nt

FIGURE 25B



GACTACAAAGACNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKAACTTCTACGACTGGTTCG
D Y K D X X X X X X X X X X N F Y D W F

TTNNKNNKNNKNNK 21 aa
V X X X X

FIGURE 26A

CTACAAAGACNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKNNKAACTTCTACGACTGGTTCGTTNNK
NNKNNKNNKGC GGCCGCAGTGTGA

FIGURE 26B



H5	NH ₂ -D-Y-K-D-L-C-Q-S-L-G-V-T-Y-P-G-W-L-A-G-W-C-A-K-K(Biotin)-COOH
H5 Control	NH ₂ -D-Y-K-D-W-C-L-T-L-Q-F-L-V-W-A-S-G-G-G-Y-C-A-K-K(Biotin)-COOH
2C3-60	NH ₂ -D-Y-K-D-V-C-Q-R-L-G-G-T-F-P-G-W-L-V-G-V-C-R-K-K(Biotin)-COOH
H5-447	NH ₂ -D-Y-K-D-L-C-Q-R-L-G-V-G-W-P-G-W-L-S-G-W-C-A-K-K(Biotin)-COOH
H5-432	NH ₂ -D-Y-K-D-L-C-Q-S-L-G-V-T-W-P-G-W-L-A-G-W-C-A-K-K(Biotin)-COOH

FIGURE 27



Clone:

Binding Ratios:
Target E-Tag % Max

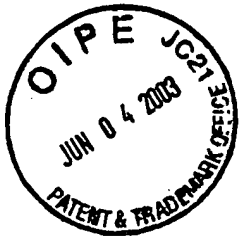
A6S-1-C5	DYKD RIHNQTERCGNFYDWFVHqLV AAA	7	27	26
A6S-1-G3	DYKD VATVHVGGGMNFYDWFVAqVG AAA	5	19	26
A6S-1-A2	DYKD KDPVTVSQGRNFYDWFVVqIQ AAA	5	20	25
A6S-1-D5	DYKD RVGSGMEDLGNFYDWFVRQAq AAA	5	25	20
A6S-1-H4	DYKD HKSWTTMSPLNFYDWFVAqVE AAA	3	18	17
A6S-2-F2	DYKD LAMSVASRPANFYDWFVAqIV AAA	30	35	86
A6S-2-D2	DYKD RAERGSMRDSNFYDWFVqQLP AAA	30	36	83
A6S-2-E3	DYKD VqEGLSGMEGNFYDWFVDQLF AAA	28	36	78
A6S-2-H2	DYKD RGqRESDSGTNFYDWFVGAIR AAA	28	40	70
A6S-2-A3	DYKD SRAPYGSTAGNFYDWFVqAVS AAA	25	37	68
A6S-2-H1	DYKD RVGIqVDPHTNFYDWFVIQLT AAA	27	42	64
A6S-2-F1	DYKD VGqVGRYVRSNFYDWFVQqAM AAA	8	30	27
A6S-2-G1	DYKD RPqLVESGSKNFYDWFVqVVR AAA	8	30	27
A6S-2-B2	DYKD EMYGDTSERVNFYDWFVSALq AAA	5	30	17
A6S-2-A1	DYKD LSSRGRVTMRNFYDWFVAqVV AAA	3	31	10
A6S-3-E10	DYKD RVREKLPRPENFYDWFVNqIH AAA	22	23	96
A6S-3-G2	DYKD TWMWEERKqDNFYDWFVGQLK AAA	20	21	95
A6S-3-E5	DYKD RYRGERHDGRNFYDWFVEqVN AAA	19	21	90
A6S-3-H2	DYKD qGAEGRLSEGNFYDWFVQAVS AAA	19	21	90
A6S-3-H9	DYKD YSIEVqDWNENFYDWFVSQLG AAA	20	23	87
A6S-3-G3	DYKD PRLHMGSDMGDFYDWFVVqIA AAA	18	21	86
A6S-3-F8	DYKD GRGqGLKRPDNFYDWFVAAAK AAA	20	25	80
A6S-3-G11	DYKD GAVGLAEAGPNFYDWFVSqVq AAA	19	24	79
A6S-3-H1	DYQD PASNKNSLAENFYDWFVqQTR AAA	23	30	77
A6S-3-E6	DYKD DARDHGVWVMSNFYDWFVAqVS AAA	5	20	25
A6S-3-D9	DYKD SLQGADFqQGNFYDWFVSELA AAA	4	17	24
A6S-3-E3	DYKD RPSLPEVRPGNFYDWFVqSVR AAA	4	19	21
A6S-3-H8	DYKD NPTSVqQYGVNFYDWFVNVLS AAA	4	20	20
A6S-3-G4	DYKD CADPGACSSLNFYDWFVqMRG AAA	4	21	19
A6S-3-B10	DYKD YDqDPPYWGLNFYDWFVREVA AAA	3	16	19
A6S-3-C1	DYKD RPIVIGGGGTRNFYDWFVAqMI AAA	3	17	18
A6S-4-G5	DYKD QEVTRTRDDKNFYDWFVSqIF AAA	26	18	144
A6S-4-D2	DYKD PPYRSSRLGENFYDWFVMqVR AAA	26	19	143
A6S-4-F6	DYKD LKGSSQPLSVNFYDWFVQQIK AAA	24	17	142
A6S-4-H4	DYKD PRMVEKPSDNFYDWFVTqLS AAA	28	20	141
A6S-4-C1	DYKD CWARPCGDAANFYDWFVqQAS AAA	22	16	141
A6S-4-G3	DYKD GAQAIREIHNFYDWFVAQVT AAA	29	21	139
A6S-4-H3	DYKD GRGDQRHETTNYDWFVRELq AAA	28	20	137

FIGURE 28



A6S-4-H5.	DYKD	GSIAQLIMRANFYDWFVEqTN	AAA	24	18	130
A6S-4-G6	DYKD	RLMGGIAEFqNFYDWFVREVA	AAA	25	20	126
A6S-4-H5	DYKD	HHSPGNEHGYNFYDWFVLqVA	AAA	24	19	123
A6S-4-E4.	DYKD	ERSAAGFREGNFYDWFVAqVN	AAA	32	27	120
A6S-4-F5.	DYKD	GSQHSGREPHNFYDWFVAqVG	AAA	28	24	120
A6S-4-D4	DYKD	IARMRETFQPNFYDWFVDQLA	AAA	21	18	118
A6S-4-C6	DYKD	RLDRSSTSGVNFYDWFVAqVG	AAA	28	25	116
A6S-4-D3	DYKD	GLRSEQGNRLNFYDWFVAQIA	AAA	23	20	116
A6S-4-F2	DYKD	SVIQTRQDETNFYDWFV?AMS	AAA	26	23	115
A6S-4-A5	DYKD	VEVQRHIRKDNFYDWFVKQID	AAA	22	19	115
A6S-4-C3	DYKD	VTMLDKGAQDNFYDWFVREVA	AAA	24	21	114
A6S-4-F3	DYKD	HNSSSPMRTGNFYDWFVQELR	AAA	30	26	113
A6S-4-B4	DYKD	ERSPRPALASNFYDWFVQQVV	AAA	21	19	113
A6S-4-B6	DYKD	SDARQAGLQENFYDWFVSQVR	AAA	26	23	113
A6S-4-B1	DYKD	RHERGKEGPGNFYDWFVSQVV	AAA	21	19	112
A6S-4-G4	DYKD	SALSGPVqPINFYDWFVTGM	AAA	30	26	112
A6S-4-A6	DYKD	HVEHMAVG DGNFYDWFVVqLR	AAA	23	21	111
A6S-4-F4	DYKD	VGHSGVPPYPNFYDWFVMQVS	AAA	24	22	110
A6S-4-D6	DYKD	LGAAETWDGINFYDWFVKQVS	AAA	24	22	110
A6S-4-E6	DYKD	RSSGGLLSqGNFYDWFVSQLE	AAA	26	24	109
A6S-4-A3	DYKD	LAINDLVTHKNFYDWFVDQLR	AAA	20	18	109
A6S-4-E3	DYKD	RGMTGMVGRGNFYDWFVGQLR	AAA	23	21	109
A6S-4-A2	DYKD	IGGQGQH QDGNFYDWFVEALA	AAA	22	20	107
A6S-4-B2	DYKD	QSVDL SRPDSNFYDWFVEVLS	AAA	22	21	105
A6S-4-H2	DYKD	VTFTSAVFHENFYDWFVRQVS	AAA	20	19	104
A6S-4-D1	DYKD	SNPSRQDASVNFYDWFVREVA	AAA	22	22	103
A6S-4-H1	DYKD	IVAGARHSEVNFYDWFVIQVR	AAA	18	18	102
A6S-4-E2.	DYKD	?DGQSVSSKGNFYDWFVQqMT	AAA	25	25	101
A6S-4-G1	DYKD	AELVGAGVRGNFYDWFVDQLV	AAA	16	16	101
A6S-4-G2	DH KD	SAGHHMPRESNFYDWFVDQVV	AAA	24	25	99
A6S-4-A1	DYKD	DSSRLWLGERNFYDWFVAqIS	AAA	12	17	68

FIGURE 28 (Cont.)



Name	Sequence	#Found	Ratio	IGF Inh.	GHR*
H5:	LCQSLGVTPGWLAWCA	-	1.2	-	2.0
2C3:	VCQRLGGTFPGWLGVCR	-	1.1	-	1.1
JBA5:	LCQSWGVRI-GWLAGLCP	19	-24.0	-45%	1.2
E2A12:	LCQSLGFTOLDWLACWFE	10	-17.5	-54	1.1
E1A11:	VCQSLGITDLGLCAGWGA	1	16.4	50	1.0
E4B10:	LCQSLGLTHPGFEAWLCA	5	-11.7	-50	1.2
E4C10:	LCQNFVGTDPGCFYGWFA	1	9.9	-51	0.7
E4A9:	LCQSSGLSFLGCL-GWWA	14	-8.5	-65	1.0
JBB6:	PCQRLGDTHLCWLAGWFA	6	-8.3	-65	1.1
E1F9:	PCQSLGLTCSGWFEWGA	1	8.3	68	1.2
E4G7:	QWQSLGVTCPGSWAELCA	1	6.0	50	1.3
E4A11:	EWQSVGIKYPGGLAGWLA	1	5.8	67	1.4
E1B9:	LCQSLGVTYWEGLAWLCA	3	5.5	60	1.1
E4A12:	VCQSLGVECPGWFAWGA	3	-5.3	-55	1.2
E4F11:	LCQGWGIRI-GWLVGRCM	1	2.7	58	1.1
E1D3:	LCQSLGVTPGWLAWGCA	1	2.0*	-	1.0

FIGURE 29



Genomic rVab Library

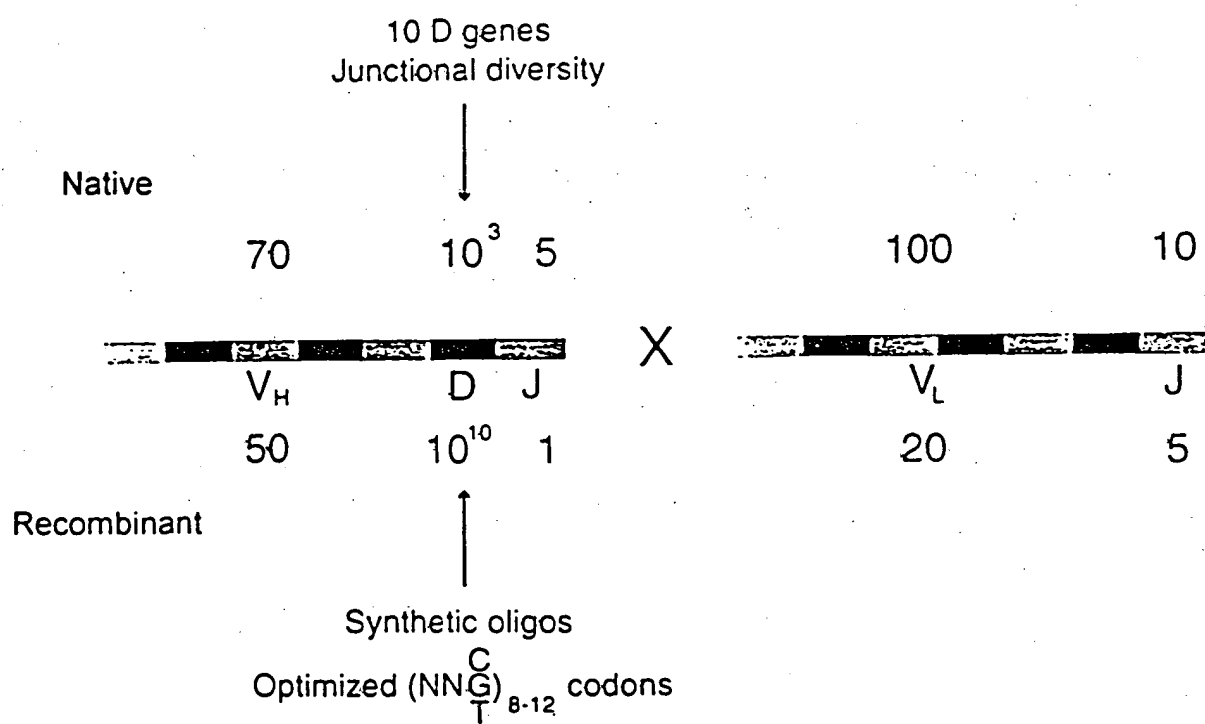


FIGURE 30



VH Gene Sequences

DP-1
DP-10
DP-12
DP-14
DP-15
DP-2
DP-21
DP-25
DP-29
DP-30
DP-31
DP-32
DP-33
DP-35
DP-38
DP-39
DP-40
DP-42
DP-44
DP-45
DP-46
DP-47
DP-5
DP-50
DP-51
DP-52
DP-53
DP-54
DP-59
DP-63
DP-66
DP-67
DP-68
DP-69
DP-7
DP-70
DP-71
DP-73
DP-74
DP-8
hv1263
VHD26

Lambda and Kappa
Gene Sequences

DPK11
DPK15
DPK18
DPK2/L14+
DPK3/L11+
DPK4
DPK6
DPK8/Vd+
DPL23
HK101
L22+
L23/L23a
LFVK431
VA++

FIGURE 31

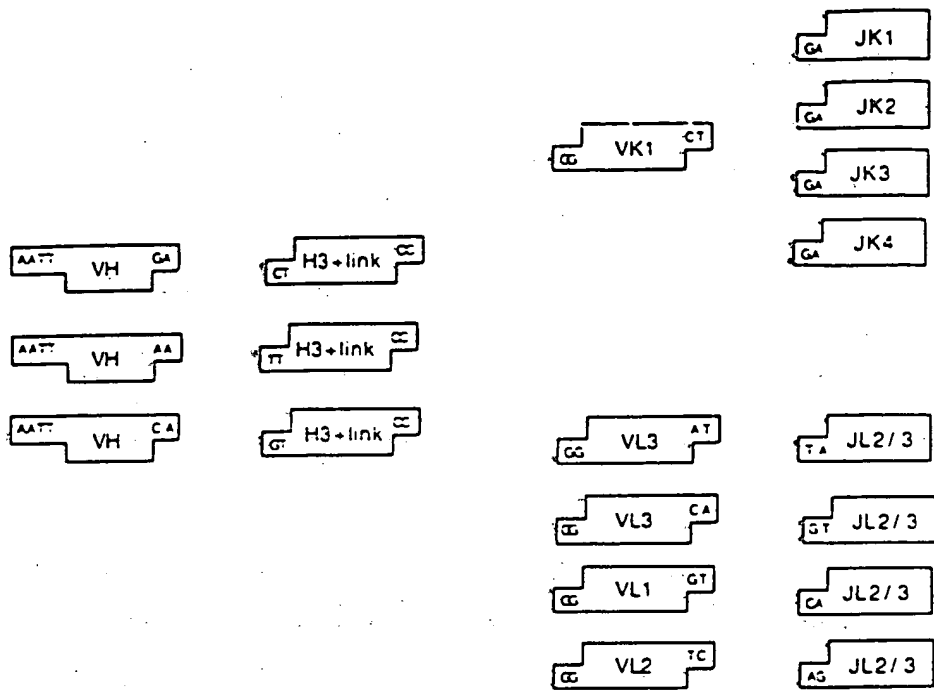


FIGURE 32



10	20	30	40	50	60														
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890														
GGCCAGGGGG	CCATGGGCCA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAAGGCT	60													
	Q	V	Q	L	V	E	S	G	G	G	L	V	K	P					
GGGGGGGGCC	TTAGACTCTC	CTGTGCAGCC	TCGTGAATCA	CTTTCAGTAA	GGCTGGGATG	120													
G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	N	A	W	M
AGCTGGGTCC	GCCAGGCTCC	AGGGAGGGGG	CTGGAGTGGG	TTGGGGGTAT	TAAAAGCAAA	180													
S	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	R	I	K	S	K
ACTGTGGTGG	GGACAACAGA	CTACGGTCCA	CCCGTGAAG	GCAGATTAC	CATCTCAAGA	240													
T	D	G	G	T	T	D	Y	A	A	P	V	K	G	R	F	T	I	S	R
GATGATTCAA	AAAACAGGCT	GTATCTGCAA	ATGACAGCC	TGAAAACCGA	GGACACAGCC	300													
D	D	S	K	N	T	L	Y	L	Q	M	N	S	L	K	T	E	D	T	A
GTGTATTACT	GTACCAAGT	TGGGTGTGCT	GCCGACGGTG	GGATGTGGGG	TCAAGGAAGT	360													
V	Y	Y	C	T	T	V	A	L	S	A	D	R	G	M	W	G	Q	G	T
CTGGTCACCG	TCTCTCAGG	TGGAGGGGGT	TCAGGGGGAG	GTGGCTCTGG	CGGTGGGGGA	420													
L	V	T	V	S	S	G	G	G	G	S	G	G	G	G	S	G	G	G	G
TCCGATGTGG	TGATGACTCA	GTCTCCACTC	TCCCTGCCCC	TCACCCCTGG	ACAGCCGGCC	480													
S	D	V	V	M	T	Q	S	P	L	S	L	P	V	T	L	G	Q	P	A
TCCATCTCCT	GCAGGCTAG	TCAAGGCTTC	GTATACAGTG	ATGGAACAC	CTACTTGAAT	540													
S	I	S	C	R	S	S	Q	S	L	V	Y	S	D	G	N	T	Y	L	N
TGGTTTCAGC	AGAGGCCAGG	CCATCTCCA	AGGGGGCTAA	TTTATAAGGT	TTCTAACCGG	600													
W	F	Q	Q	R	P	G	Q	S	P	R	R	L	I	Y	K	V	S	N	R
GACTCTGGGG	TCCCAGACAG	ATTCAGGGCC	AGTGGGTGAG	GCACTGATTT	CACACTGAAA	660													
D	S	G	V	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	K
ATCAGCAGGG	TGGAGGCTGA	GGATGTGGGG	GTTEATTACT	GCATGCAAGG	TACACACTGG	720													
I	S	R	V	E	A	E	D	V	G	V	Y	Y	C	M	Q	G	T	H	W
CCTTACACTT	TTGGGCAGGG	GACCAAGCTG	GAGATCAAG	GGGGGGC		767													
P	Y	T	F	G	Q	G	T	K	L	E	I	K							

FIGURE 34



10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCGG	CCATGGCCCA	GATGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAGCCCT	60
	Q	M Q L	V E S G	G G L	V K P	
GGGGGTCCTC	TTAGACTCTC	CTGTGACGCC	TC'GGATYCA	CTTTCAGTAA	GGCTCGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GGCAGGCTCC	AGGGAGGGGG	CTGGAGTGGG	TTGGGGTAT	TAAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGCAACAGA	CTACGGTCCA	CCCGTGAAG	GCAGATTCA	CATCTCAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCAA	AAAACAGCT	GTATCTGCAA	ATGACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTGTATTACT	GTACCACATG	GGGCTCCGTC	GACACGGACA	ACTACGCCAG	GTTTTGGGGT	360
V Y Y C	T T W	G S V	D T D N	Y A R	F W G	
CAAGCACTC	TGGTCACCGT	CTCTCAGGT	GGAGGGGGTT	CAGGGGGAGG	TGGCTCTGGC	420
Q G T L	V T V	S S G	G G G S	G G G	G S G	
GGTGGGGGTT	CCGACATCCA	GATGACCCAG	TCTCCATCCT	CCCTGTCTGC	ATCTGTAGGA	480
G G G S	D I Q	M T Q	S P S S	L S A	S V G	
GACAGACTCA	CCATCACTTG	CCGGGGGGGT	CAGGGGATTA	GCAATTATTT	AGCTTGGTAT	540
D R V T	I T C	R A S	Q G I S	N Y L	A W Y	
CAGCAGAAC	CAGGCAAGT	TCTTAAGCTC	CTGATCTATG	CTGCATCCAC	TTTGCAATCA	600
Q Q K P	G K V	P K L	L I Y A	A S T	L Q S	
GGGGTCCCAT	CTGGGTTGAG	TGGCAGTGGG	TCTGGGACAG	ATTTCAGTCT	CACCATCAGC	660
G V P S	R F S	G S G	S G T D	F T L	T I S	
AGCTGCAGC	CTGAGATGT	TGCAACTTAT	TACTGTCAAA	AGTATAACAG	TGCGGCTCTC	720
S L Q P	E D V	A T Y	Y C Q K	Y N S	A P L	
ACTTTGGGGG	GAGGGACCAA	GGTGGAGATC	AAAGCGGGCG	C		761
T F G G	G T K	V E I	K			

FIGURE 35



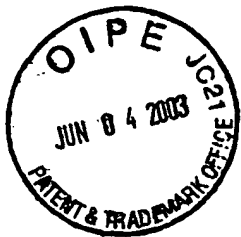
10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCCCG	CCATGCCCCA	GATGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAAGGCT	60
	Q	M Q L	V E S G	G G L	V K P	
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCGTGATTCA	CTTTCAGTAA	GGCCTGGATG	120
G G S L	R L S	C A A	S G F T	F S N	A W M	
AGCTGGGTCC	GGCAGGCTCC	AGGGAGGGGG	CTGGAGTGGG	TTGGGGGTAT	TAAAGCAAA	180
S W V R	Q A P	G K G	L E W V	G R I	K S K	
ACTGATGGTG	GGACACAGA	CTAGGCTGCA	CCCGTGAAAG	GCAGATTCA	CATCTCAGA	240
T D G G	T T D	Y A A	P V K G	R F T	I S R	
GATGATTCPA	AAAACAGGCT	GTATCTGCPA	ATGACAGCC	TGAAAACCGA	GGACACAGCC	300
D D S K	N T L	Y L Q	M N S L	K T E	D T A	
GTGTATTACT	GTACCACACC	GGGCTGGTAT	GGGGCCGAGG	ATAAGTGGGG	TCAAGGA	360
V Y Y C	T T P	G W Y	G A E D	K W G	Q G T	
CTGGTCACCG	TCCTCTCAGG	TGGAGGGGGT	TCAGGGGGAG	GTGGCTCTGG	GGTGGGGGA	420
L V T V	S S G	G G G	S G G G	G S G	G G G	
TCCGATATCC	AGATGACCCA	GTCTCCATCC	TCCTGTCTTG	CATCTGTAGG	AGACAGAGTC	480
S D I Q	M T Q	S P S	S L S A	S V G	D R V	
ACCATCACTT	GGGGGGGGAG	TCAGGGGCTT	AGCATATATT	TAGGCTGGTA	TCAGCAGAAA	540
T I T C	R A S	Q G I	S N Y L	A W Y	Q Q K	
CCAGGGAAAG	TTCTTAAGCT	CCTGATCTAT	GCTGCAATCA	CTTTGCAATC	AGGGGTCCCA	600
P G K V	P K L	L I Y	A A S T	L Q S	G V P	
TCCTGGTTCA	GTGGCAGTGG	ATCTGGGACA	GATTTCATCT	TCACCATCAG	CAGGCTGCAG	660
S R F S	G S G	S G T	D F T L	T I S	S L Q	
CCTGAAGATG	TTGCAACTTA	TTACTGTCAA	AAGTATAACA	GTGGGGCTTT	CACCTTGGGC	720
P E D V	A T Y	Y C Q	K Y N S	A P F	T F G	
CCTGGGACCA	AAGTGGATAT	CAAGGGGGCC	GC			752
P G T K	V D I	K				

FIGURE 36



10	20	30	40	50	60														
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890														
GGCCAGCGGG	CCATGGGCCA	GGTGCAGCTG	GTCGAGTCTG	GGGGAGGCTT	GGTACAGCCT	60													
	Q	V	Q	L	V	E	S	G	G	G	L	V	Q	P					
GGGGATKUC	TGAGACTCTC	CTGTGCAGGC	TCTGGATKCA	CCCTCAGTAA	CAGTGACATG	120													
G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	N	S	D	M
AATCGGGTCC	ATCAGGCTCC	AGGAAAGGGG	CTGGAGTGGG	TATCGGGTGT	TAGTTGGANT	180													
N	W	V	H	Q	A	P	G	K	G	L	E	W	V	S	G	V	S	W	N
GGCATGGA	CGCATATGC	AGATCTCTGT	AAGGGCGGAT	TCATCATCTC	CAGAGACAT	240													
G	S	R	T	H	Y	A	D	S	V	K	G	R	F	I	I	S	R	D	N
TCCAGGACA	CCCTGTATCT	GCAAGCAAT	AGCTGAGGG	CCGAGGACAC	GGCTGTGTAT	300													
S	R	N	T	L	Y	L	Q	T	N	S	L	R	A	E	D	T	A	V	Y
TACTGTGTGA	GAGCGATGG	CGATGGTAC	GGGGCTGGG	GTCAGGAAC	TCTGGTCACC	360													
Y	C	V	R	T	D	G	E	W	Y	G	A	W	G	Q	G	T	L	V	T
GTCTCTCAG	GTGGAGGGGG	TTCAGGGGA	GGTGGCTCTG	GGGTGGGGG	ATCGGCGATC	420													
V	S	S	G	G	G	G	S	G	G	G	S	G	G	G	G	S	A	I	
CAGATGACCC	AGTCTCCATC	CTCCCTGTCT	GCTCTGTAG	GAGACAGAT	CACCATCAT	480													
Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T
TGCGGGGGCA	GTCAGGGCAT	TAGAAATGAT	TTAGGCTGGT	ATCAGGAGA	ACGAGGGAA	540													
C	R	A	S	Q	G	I	R	N	D	L	G	W	Y	Q	Q	K	P	G	K
GGCCCTAGC	TCCGGATCTA	TGCTGCATCC	AGTTTACAAA	GTCGGGTCCC	ATCAAGGTTC	600													
A	P	K	L	R	I	Y	A	A	S	S	L	Q	S	G	V	P	S	R	F
AGCGGAGTG	GATCTGGCAC	AGATTTCAT	CTCACCATCA	GCAGGCTGCA	GGCTGAAGAT	660													
S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	P	E	D
TTTGCACCTT	ATTACTGTCT	ACAAGATTAC	AATTACCCCTC	TCACCTTGGG	CGGAGGGACC	720													
F	A	T	Y	Y	C	L	Q	D	Y	N	Y	P	L	T	F	G	G	G	T
AAGGTGGGA	TCAAAGGGGC	GGC				743													
K	V	E	I	K															

FIGURE 37



10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGGCGG	GCATGGGGCA	GATGCAGCTG	GTGCAGTCTG	GGGGAGGCTT	GGTACAGGCT	60
	Q	M Q L	V Q S G	G G L	V Q P	
GGGGGTC	TCAGACTCTC	CTGRGAGGC	TCGGAATCA	CCTTCAGTAG	CTAAGCTATG	120
G G S L	R L S	C A G	S G F T	F S S	Y A M	
CACTGGGTTC	GGCAGGCTCC	AGGAAAAGGT	CTGGAGTGGG	TATCAGCTAT	TGGTACTGGT	180
H W V R	Q A P	G K G	L E W V	S A I	G T G	
GGTGGACAT	ACTATGCAGA	CTCCGTGAAG	GGCCGATTC	CCATCTCCAG	AGACATGGCC	240
G G T Y	Y A D	S V K	G R F T	I S R	D N A	
AACTACTCCT	TGTATCTTCA	ATTGACAGC	CTGAGAGCGG	AGGACATGGC	TGTGTATTAC	300
K N S L	Y L Q	M N S	L R A E	D M A	V Y Y	
TGTGCAGAT	GGGGGCAGT	CGGCTTGTGG	GTTCGGGACG	TCTATTGGGG	TCAGGGAATC	360
C A R W	G H V	G L W	V A D V	Y W G	Q G T	
CTGGTCACCG	TCTCTCAGG	TGGAGGGCGT	TCAGGGGGAG	GTGGCTCTGG	CGGTGGGGGA	420
L V T V	S S G	G G G	S G G G	G S G	G G G	
TCCGACATCC	AGATGACCA	GTCTCATCC	TCCCTGTCTG	CATCTGTAGG	AGACAGATTC	480
S D I Q	M T Q	S P S	S L S A	S V G	D R V	
AGCATCACTT	GGGGGGCGAG	TCAGGGCAAT	AGCAATATT	TAGGCTGGTA	TCAGCAGAA	540
T I T C	R A S	Q G I	S N Y L	A W Y	Q Q K	
CCAGGGGAAG	TTCCTAAGCT	CCTGATCTAT	GCTGCATCCA	CTTTGCATTC	AGGGGTCCCA	600
P G K V	P K L	L I Y	A A S T	L Q S	G V P	
TCTCGGTTC	GTGGCAGTGG	ATCTGGGACA	GATTTCACTC	TCACCATCAG	CAGGCTGCAG	660
S R F S	G S G	S G T	D F T L	T I S	S L Q	
CCTGAGATG	TTCGAATTA	TACTGTCAA	AAGTATAACA	GTGGCGCTTA	CACITTTGGC	720
P E D V	A T Y	Y C Q	K Y N S	A P Y	T F G	
CAGGGGACCA	AGCTGGAGAT	CAAAGCGGCC	GC			752
Q G T K	L E I	K				

FIGURE 38



10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCAGCGGG	CCATGGCCCA	GATGCAGCTG	GTGCAGTCTG	GGGGAGGCTT	GGTACAGGCT	60
	Q	M Q L	V Q S G	G G L	V Q P	
GGGGGGTCCC	TCAGACTCTC	CTGTGCAGGC	TCTGGATTCA	CCTTCAGTAG	CTATGCTAIG	120
G G S L	R L S	C A G	S G F T	F S S	Y A M	
CACTGGGTTC	GCCAGGCTCC	AGGAAAAGGT	CTGGAGTGGG	TATCAGCTAT	TGGTACTGGT	180
H W V R	Q A P	G K G	L E W V	S A I	G T G	
GGTGGCAGAT	ACTATGCAGA	CTCGGTGAG	GGCCGATTCA	CCATCTCCAG	AGACAATGCC	240
G G T Y	Y A D	S V K	G R F T	I S R	D N A	
AAGACTCCT	TGTATCTTCA	AATGACAGC	CTGAGAGCCG	AGGACATGCC	TGTGTATTAC	300
K N S L	Y L Q	M N S	L R A E	D M A	V Y Y	
TGTGCAGAG	AGGGGGAGCT	CGGGGTGACC	TCCTTCTGGG	GTCAAGGAAC	TCTGGTCACC	360
C A R E	G E L	G V T	S F W G	Q G T	L V T	
GTCTCTCAG	GTGGAGGCGG	TTCAGGGCGA	GGTGGCTCTG	GGGGTGGGGG	ATCCGACATC	420
V S S G	G G G	S G G	G G S G	G G G	S D I	
CAGATGACC	AGTCTCCATC	CTCGCTGTCT	GCATCTGTAG	GAGACAGAGT	CACCATCACT	480
Q M T Q	S P S	S L S	A S V G	D R V	T I T	
TGCGGGGGGA	GTGAGGGCAT	TAGCAATAT	TTAGGCTGGT	ATCAGCAGAA	ACCAGGGGAA	540
C R A S	Q G I	S N Y	L A W Y	Q Q K	P G K	
GTTCCTAAGC	TCTGATCTA	TGCTGCATCC	ACTTTGCAT	CAGGGGTCCC	ATCTGGGTTC	600
V P K L	L I Y	A A S	T L Q S	G V P	S R F	
AGTGGCAGTG	GATCTGGGAC	AGATTTCACT	CTCACCATCA	GCAGGCTGCA	GGCTGAAGAT	660
S G S G	S G T	D F T	L T I S	S L Q	P E D	
GTTCGAACIT	ATTACTGTCA	AAAGTATAAC	AGTGGCCCTT	GGAGGTGGG	GCAAGGGACC	720
V A T Y	Y C Q	K Y N	S A P W	T F G	Q G T	
AAGGTGGAAA	TCAAAGGGGC	GGC				743
K V E I	K					

FIGURE 39



A405

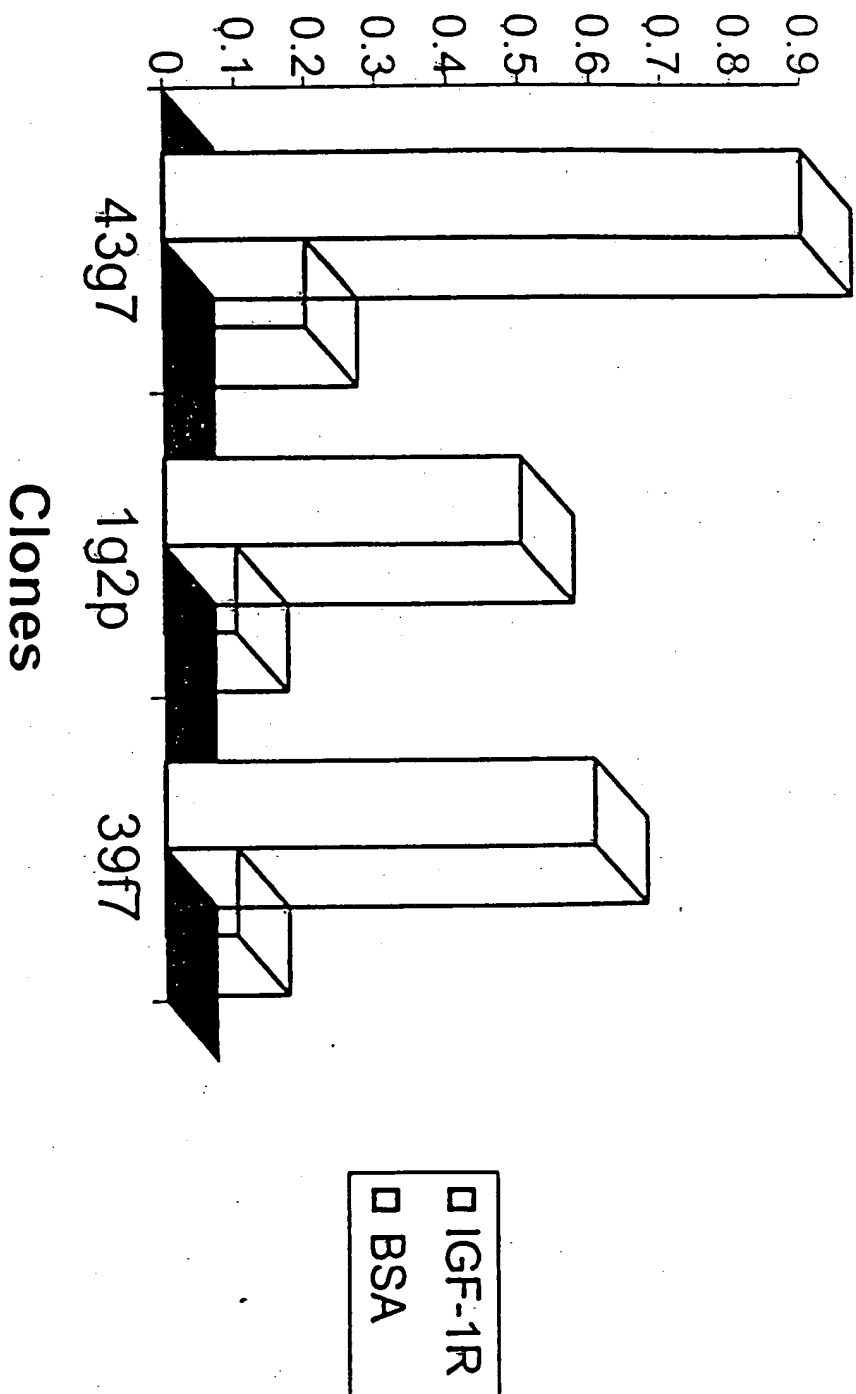


FIGURE 40

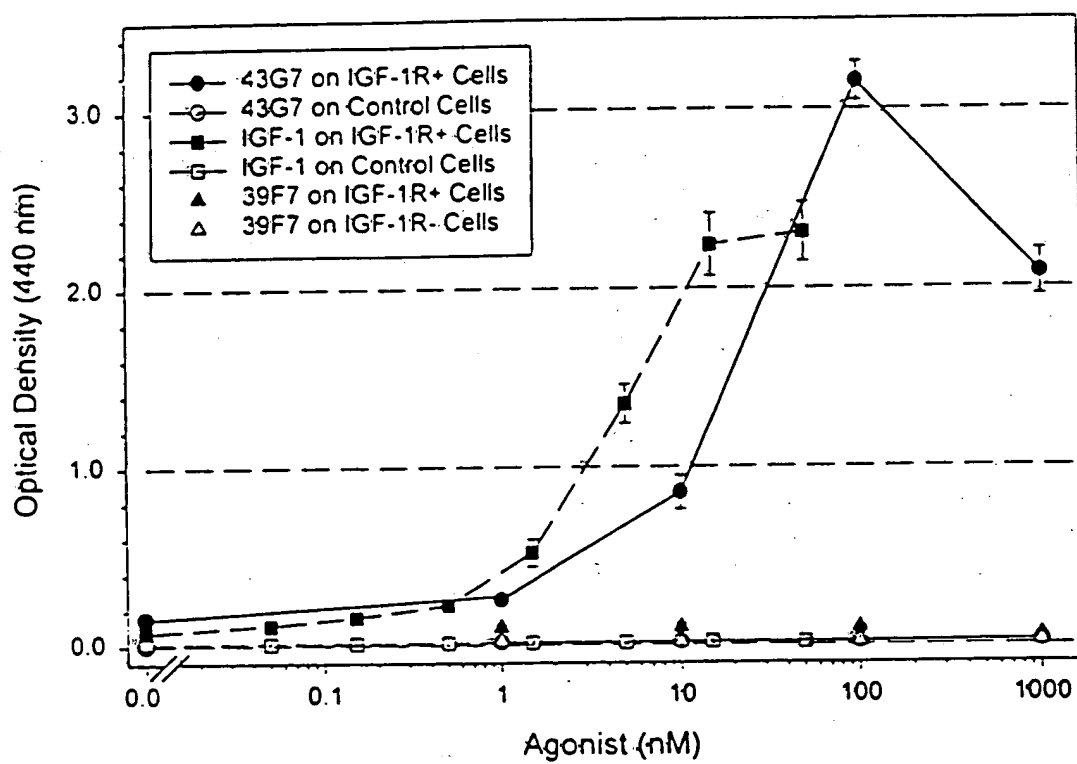


FIGURE 41

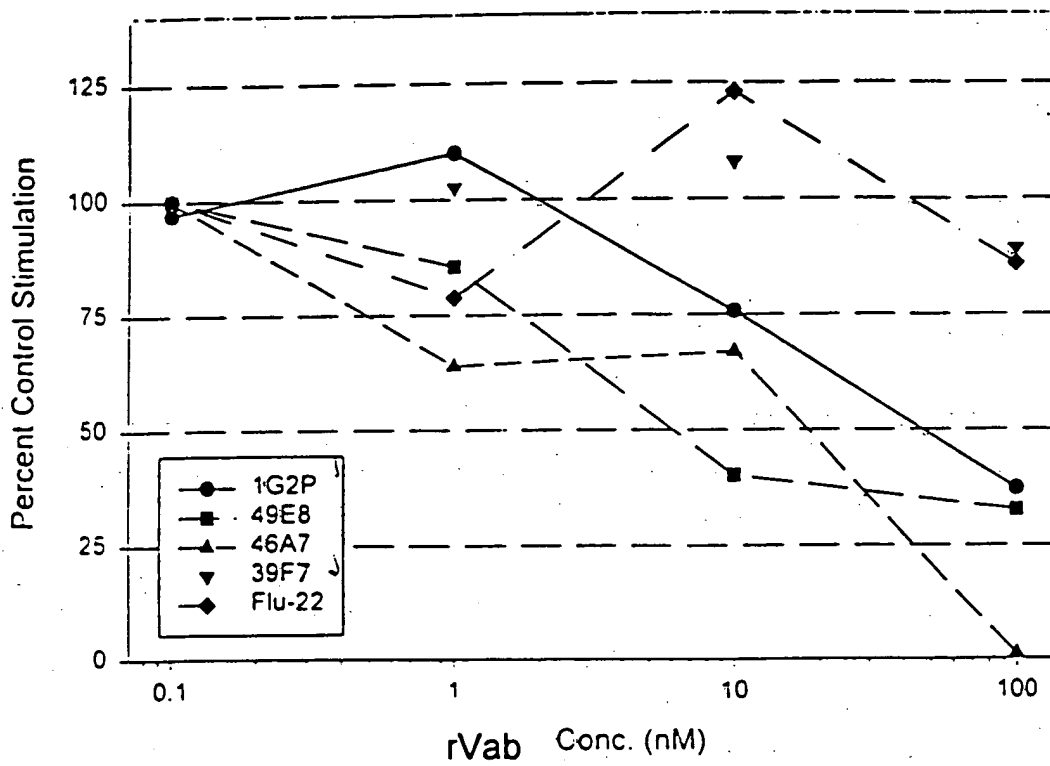


FIGURE 42

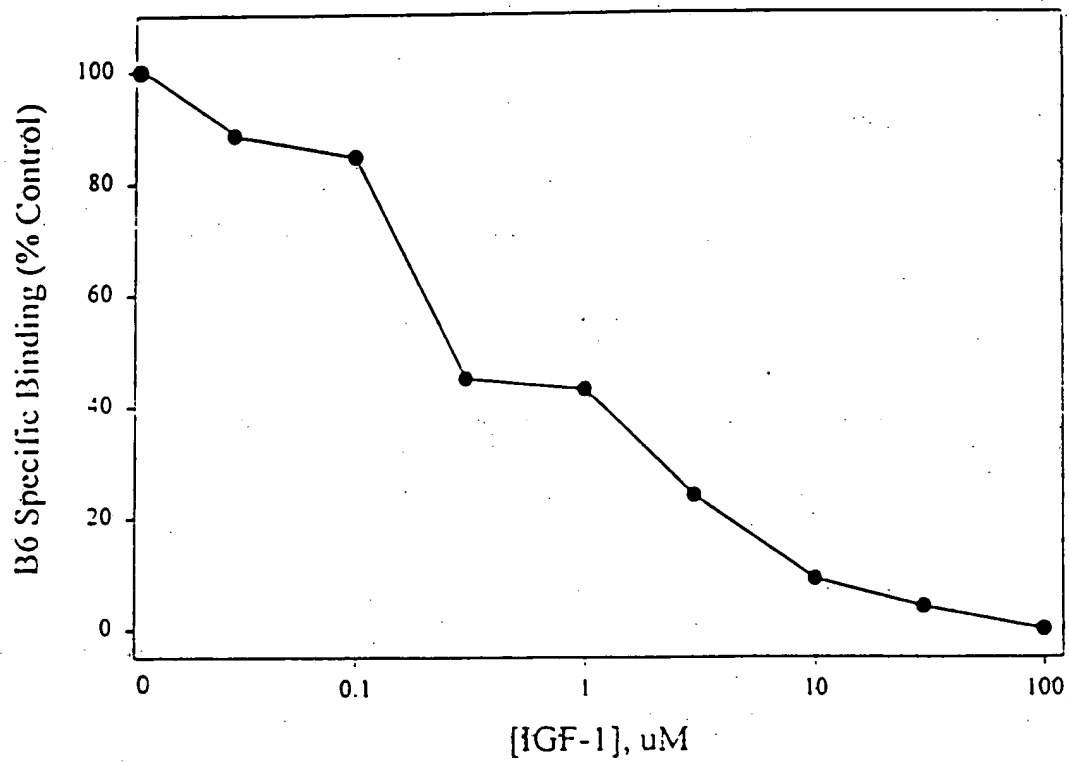


FIGURE 43

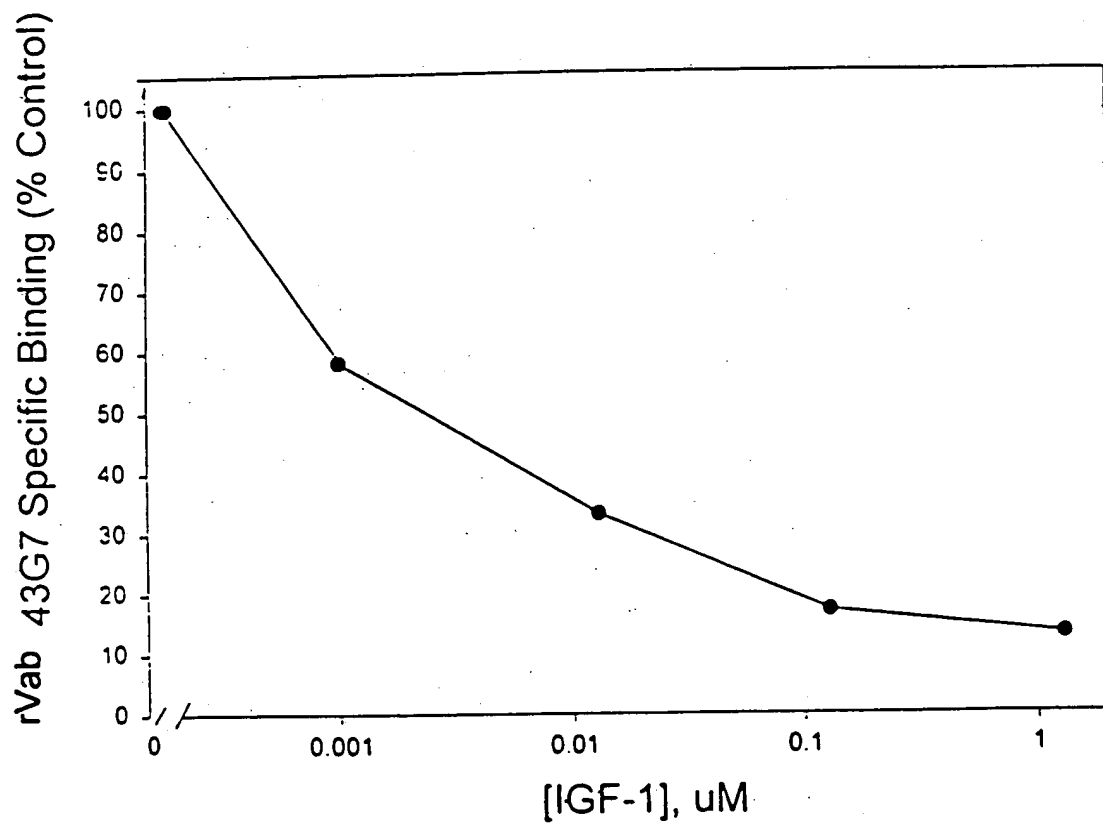


FIGURE 44

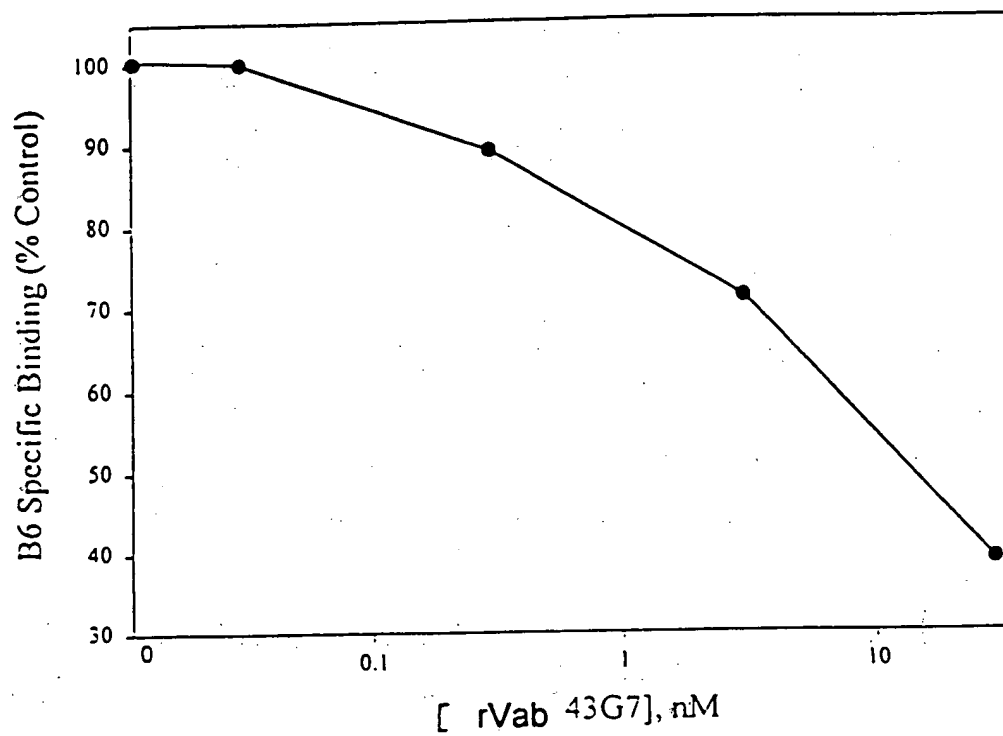
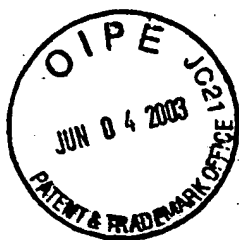


FIGURE 45



FIGURE 46A

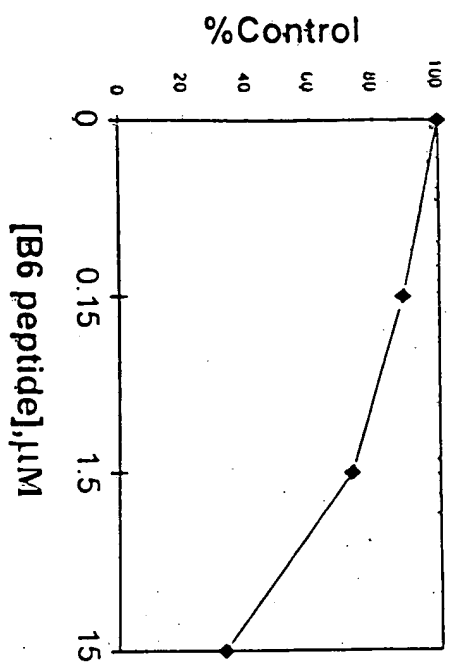


FIGURE 46B

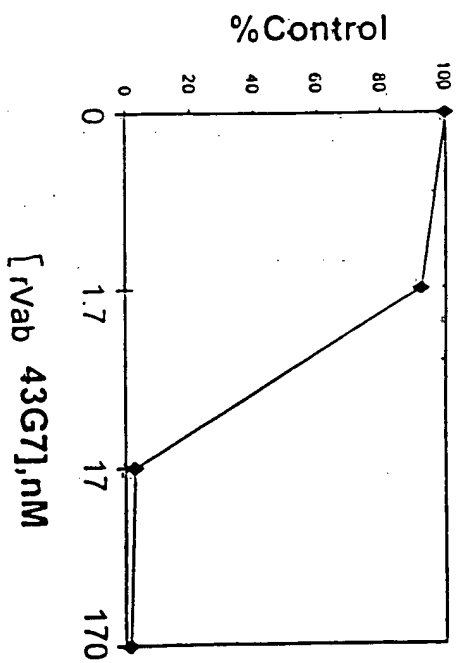


FIGURE 46C

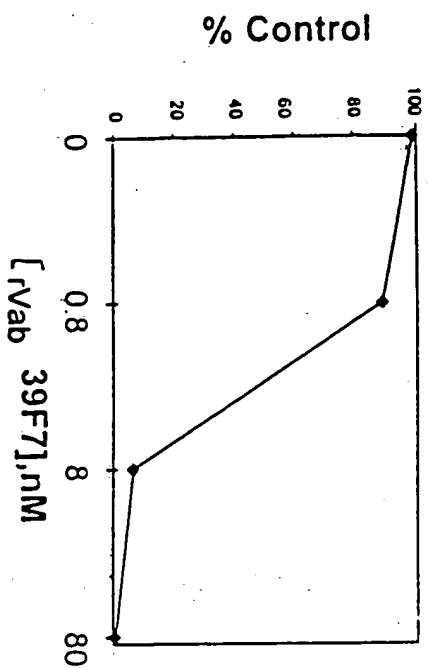
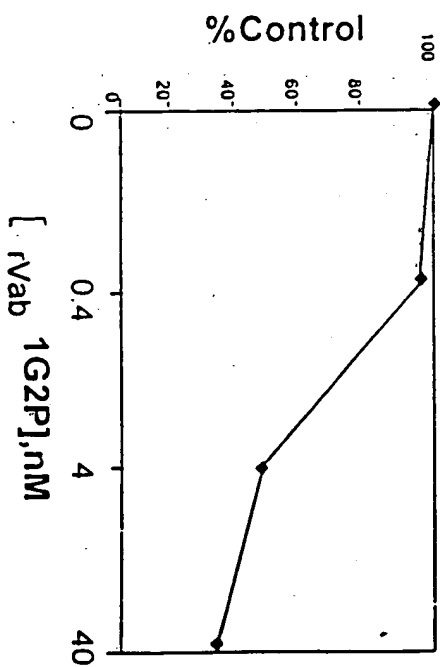


FIGURE 46D





Group 1: Formula 1 Motif		Target		
		Found	IR	IGF
20D3*	IGGQGHQDGNFYDWEVELA	18	+	++++
20F1	VEWNCRSQQLDYEWEQAA	16	+	++++
G3	RGCGTYEWEESALRKHGAG	8	+	+++
20111	RVAGALISAPGLVSNKQDGLFYSWERE	5	+	+++
20D1*	VLQNRIGCDSDCFYEMFA	4	+	+++
D2	DPERMQSDVGFYEMERAVG	3	+	+++
BS,	WSALLSVMDTGFYAWEDDAV	2	++	+++
C4	DIGSDGHRWDSFYRWEEEM	2	+	+++
A8	IGGSFVEFYGWENDQV	2	+	+++
E7,	GHSWALVRHVDRLFYEMEDL	1	++	+++
C8	LPAGGAQGFVARGFYEWEEES	1	+	+++
118	RDKPTDQEEQNMSEFYEMERII	1	+	+++
E2	SRDQNTFTNSAGFYGWEEER	1	+	+++
112	GAFTYRWHEHALVGSERVPDV	1	+	+++
D10-2	RIGGWARSEGEFYEWREEL	1	+	++
G8	RMEFYEWFSOMGAGPTGSA	1	+	++
113	HEAFYDWFSAVDGGEELMG	1	+	++
3G11	FYGWESRQLSLTPRDDWGCLP	1	+	++
F4	GVGTLTMSSDAFTWV	1	+	+
E7-2	LGTSAGQGVGIRAFYQWQOS	1	+	+
40G11	-----AALDRLEYSMES	3	+	+++
40H2	<---ETLESXYVVVQ-----	2	+	++
40B12	IRDMHYVWVQDNRDRYINGVRQWYISDRYNPGSAFYRWFTID	1	+	++
	RMGLQALAHYRKSA-----GPIFLSSGSVIKSGEDPEYAMERLQ	1	+	++

FIGURE 47

Group 2: **Formula 6 Motif**
 20A4* FIEAEWGPRVRCI.VYGRGVCG
 DS WLDQEWAMWQCFVYGRGCP

Target		
Found	IR	IGF
13	+++	0
3	+++	?

Group 3: **Formula 2 Motif**
 20E2 DYKDEYDAIDQLVRSARAGTRD
 20C11 DYKDRRAEYNGLRDLVCAVYGAMD
 20A12 DYKDRLEYCGIQALCANLGYSQCV
 C6 DYKDEYSALMGICGVTGCG
 A6 RGQSDAEFYSGLMALIGLSDG

Target		
Found	IR	IGF
1	+	++++
1	+	++++
1	+	++++
1	+	+++
1	+	+++

Group 5: **Miscellaneous Motif 10**
 D9-2 PFGFCGRWGT PPRMWRNS
 114 WWMGGRNRWMLFRWGLGGER

Target		
Found	IR	IGF
1	++	++
1	+	+

Group 4 and 6: **Miscellaneous Motif 10**
 D10 LGPLLRMGSEVCGVWPDLC
 F2 SMFVAGSDRMPCYGVLDWL
 F3 VRGFGCTVMPGYEWRNAA
 A2 GRVALMGFWMPRWRWMSRPV
 A4 WPGYLFEFEALQDWRGCTED

Target		
Found	IR	IGF
3	++	0
1	++	++
1	++	?
1	++	+
1	0	+++

Group 7: **Formula 4 Motif**
 F8 IIIICVLEFLFWGASLFGYCSG
 W6 ACSSFEVKGPEGFLQCLGSI
 40D6 PERGRCGLRTAMQIMRRTRDMLIFPHSLFWGAPPLSG

Target		
Found	IR	IGF
4	+++	+
1	0	++
1	0	0

Group 8: **Non-Aligning
 Miscellaneous
 Sequences**

FIGURE 48





FIGURE 49A

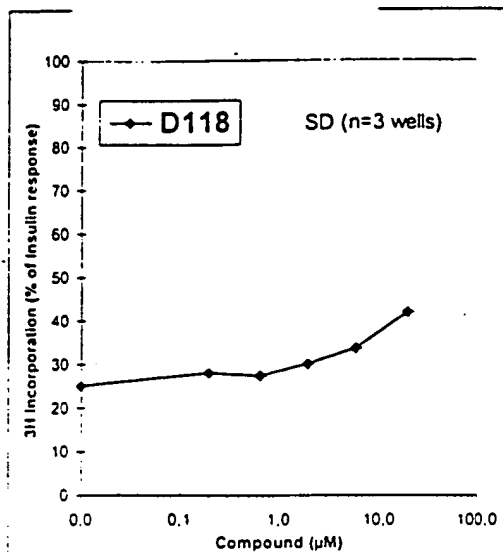


FIGURE 49B

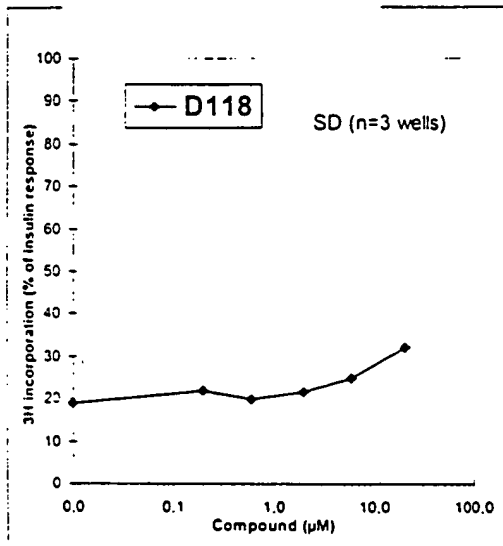
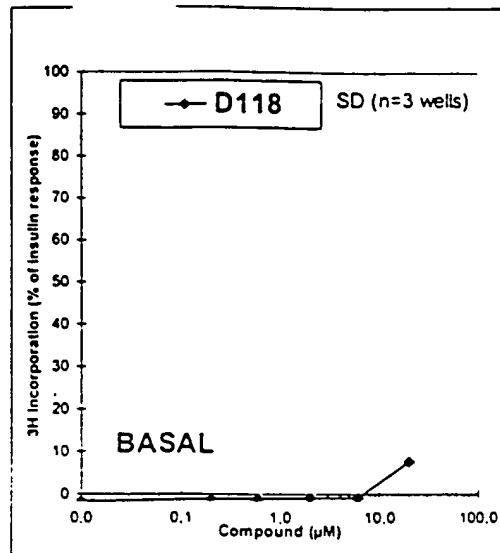


FIGURE 49C

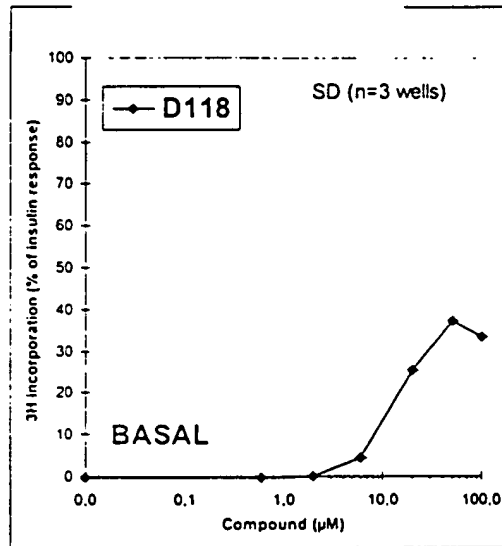


FIGURE 49D



FIGURE 50A

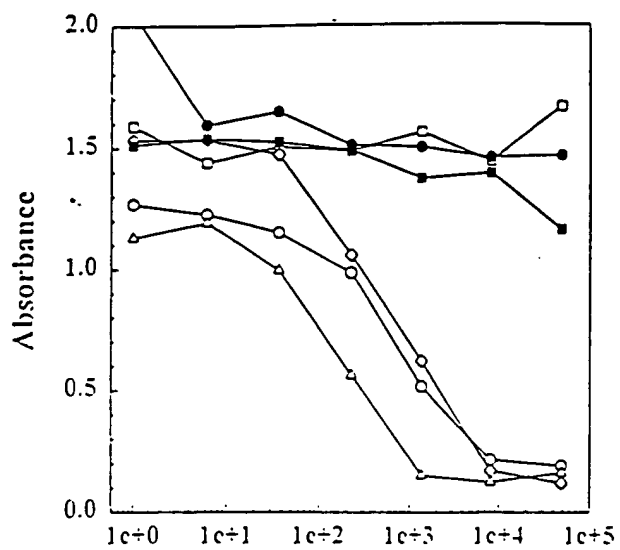


FIGURE 50B

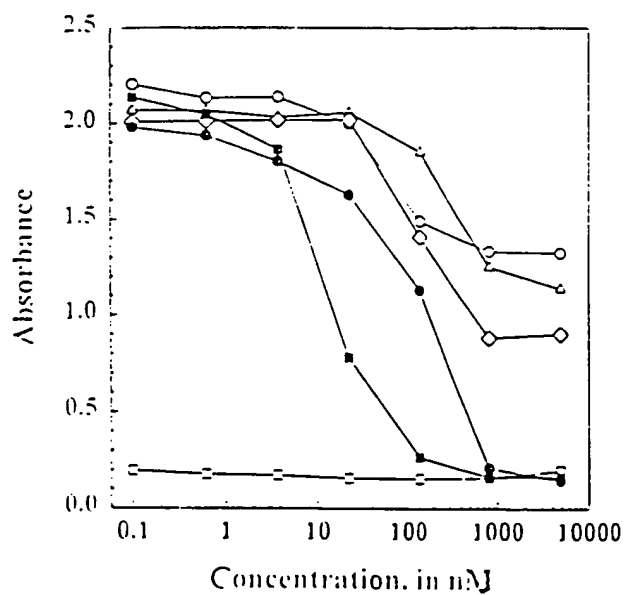
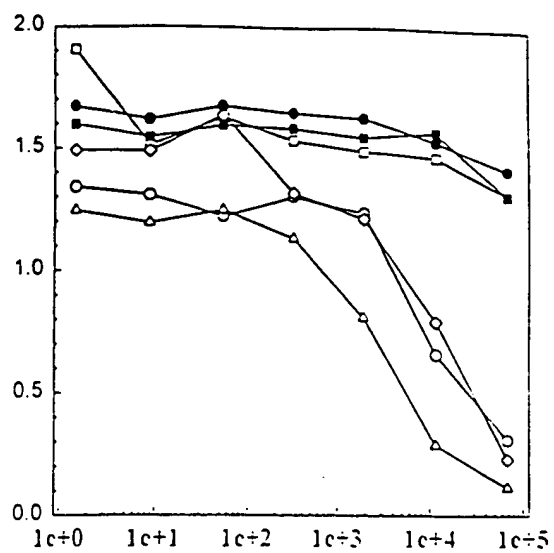


FIGURE 50C

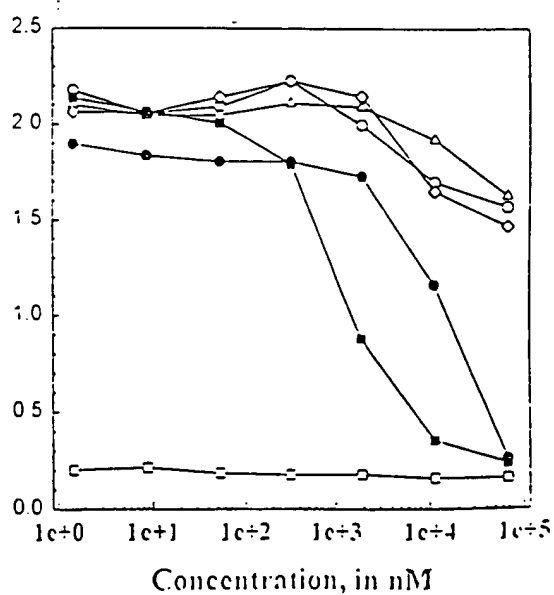


FIGURE 50D



FIGURE 51A

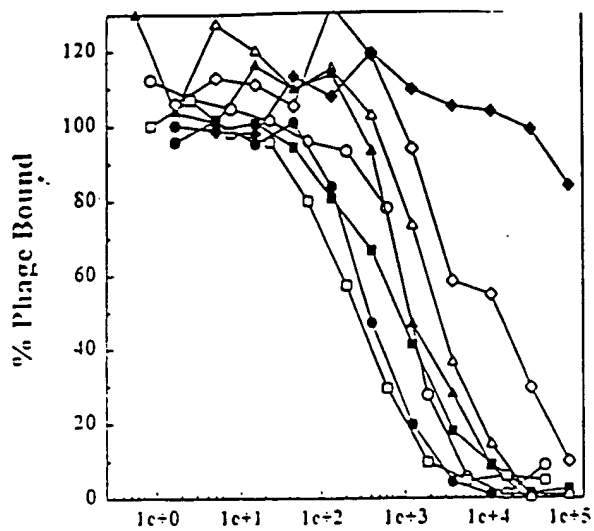
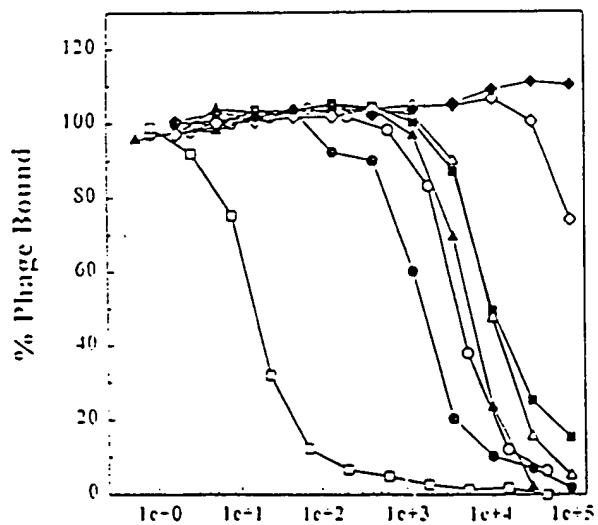
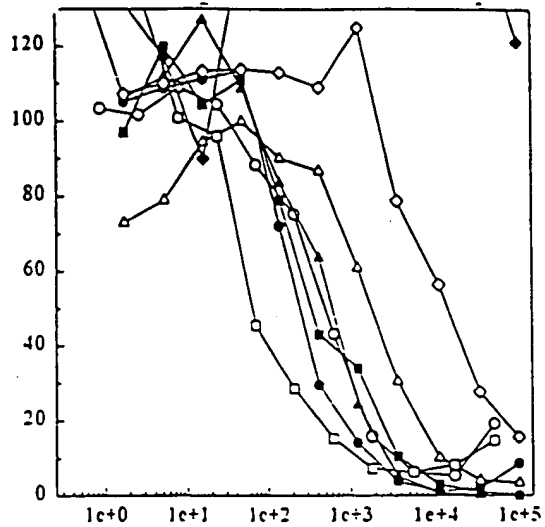
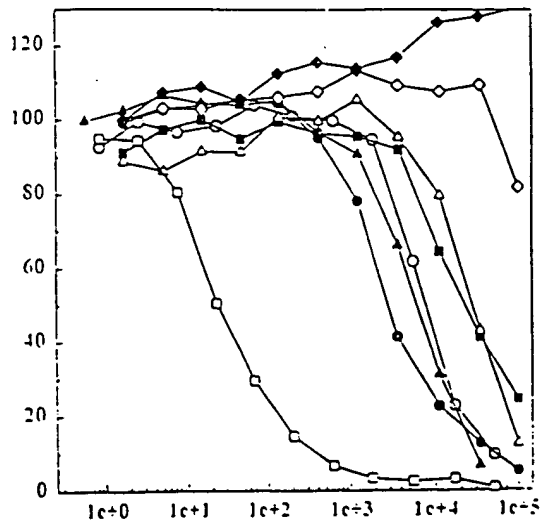


FIGURE 51B



Concentration, in nM

FIGURE 51C



Concentration, in nM

FIGURE 51D



FIGURE 52A

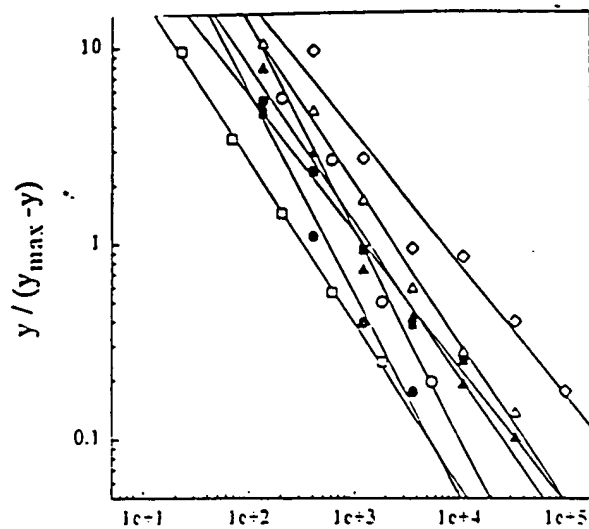


FIGURE 52B

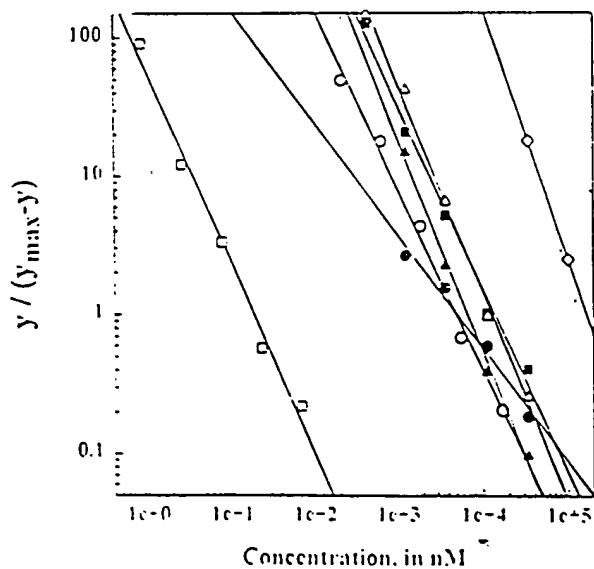
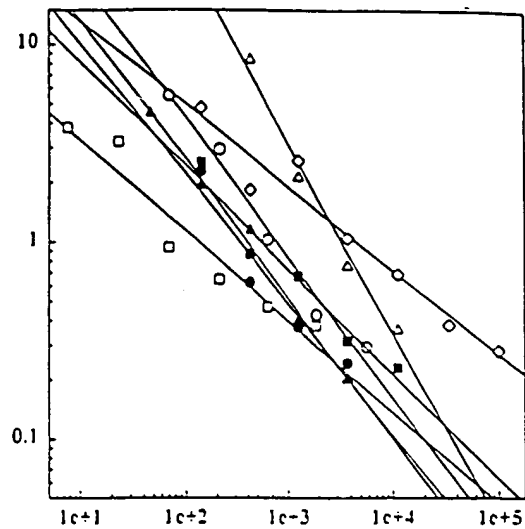


FIGURE 52C

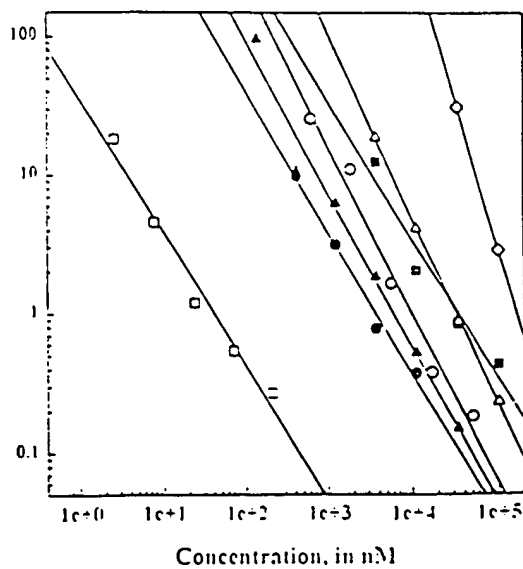


FIGURE 52D

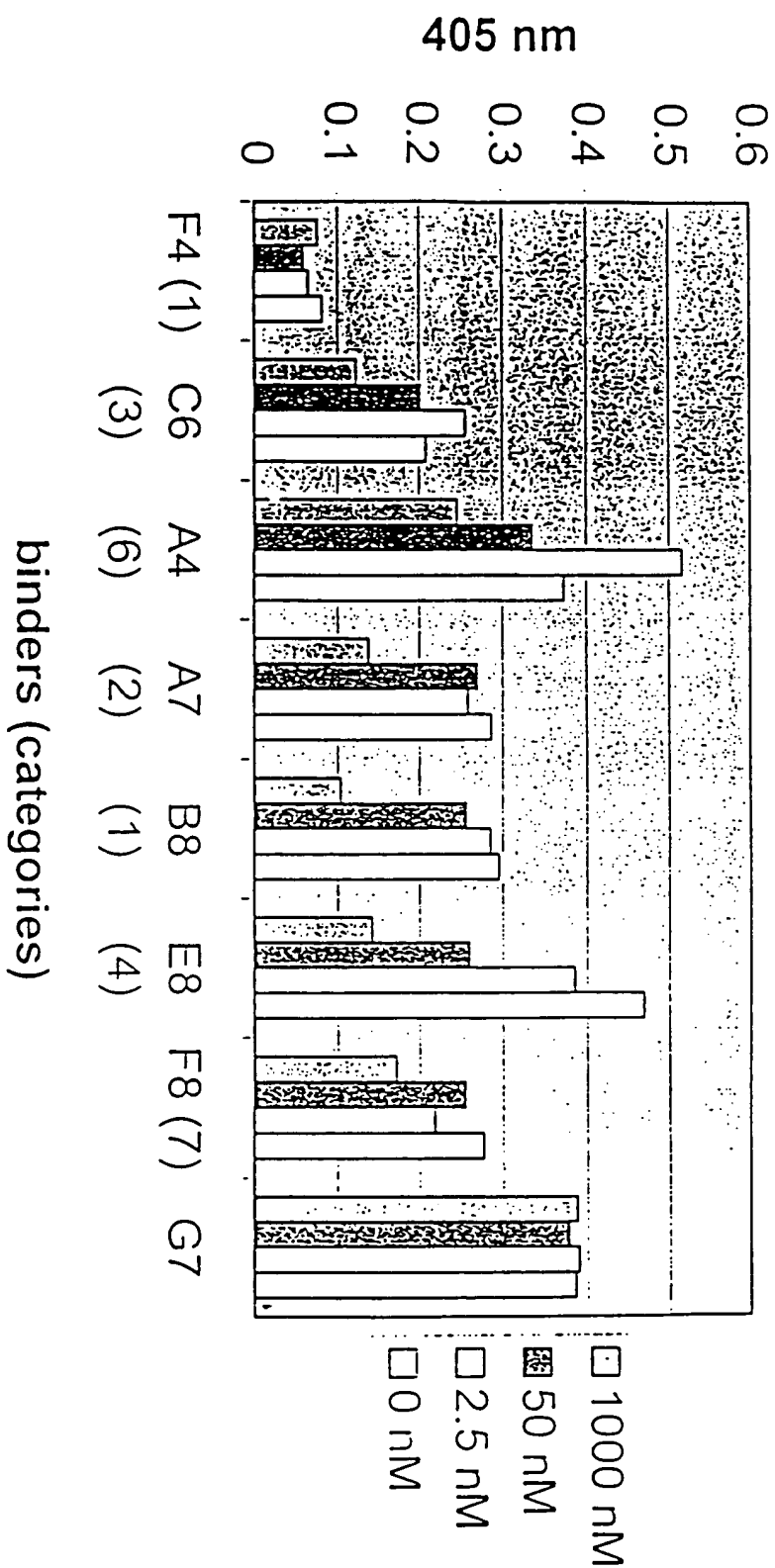


FIGURE 53

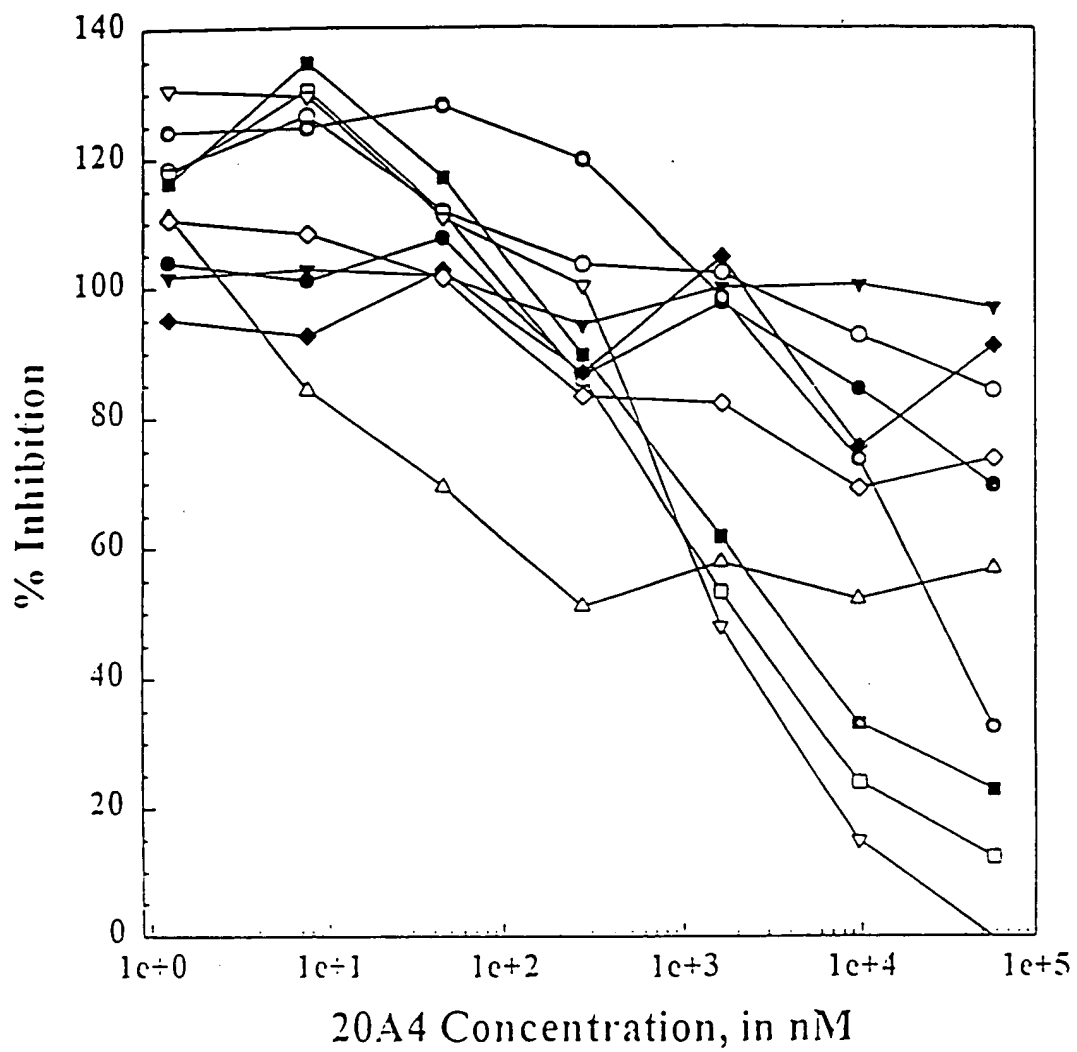


FIGURE 54

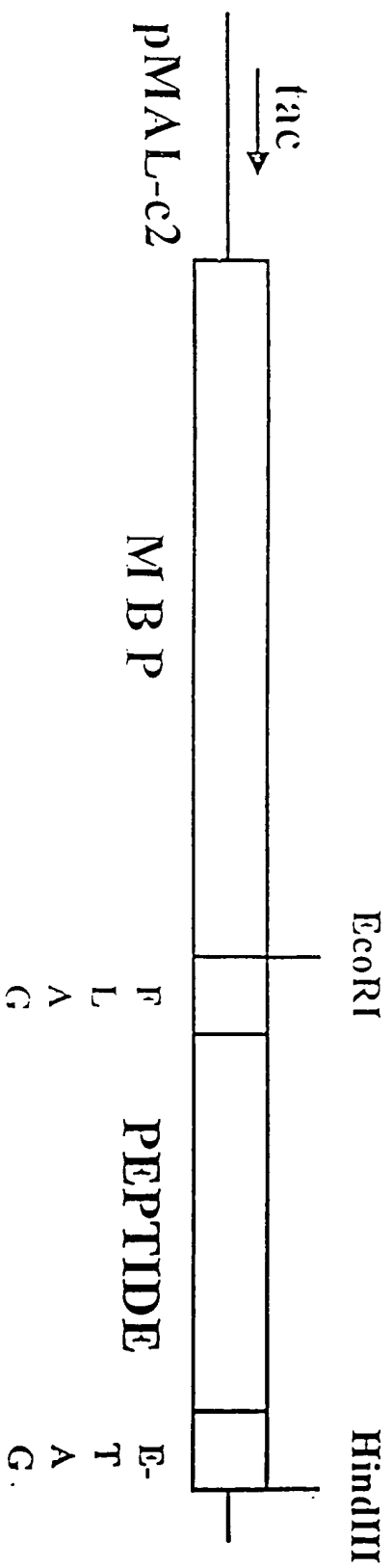


FIGURE 55



FIGURE 56A

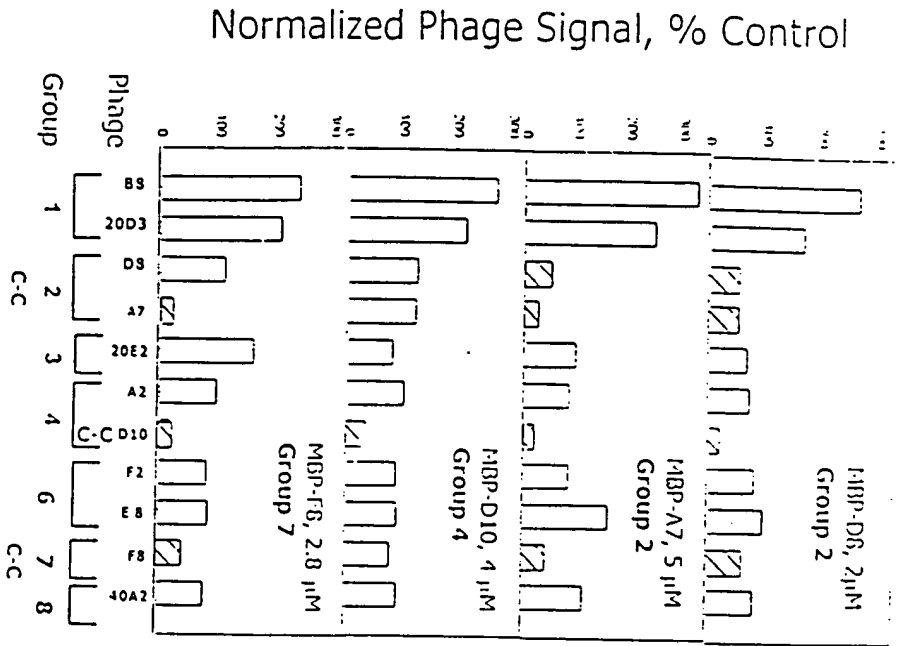


FIGURE 56B

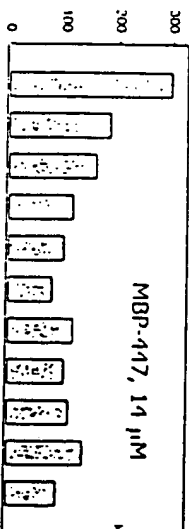
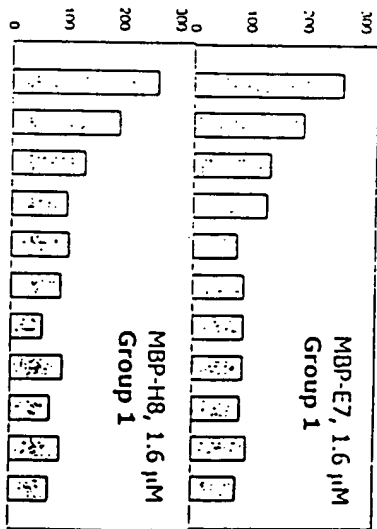


FIGURE 56C



10	20	30	40	50	60														
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890														
GGCCAGCCCG	CCATGGCCGA	GGTGCAGCTG	GTGGAGTCTG	GGGGAGGCTT	GGTAAAGCCT	60													
	E	V	Q	L	V	E	S	G	G	G	L	V	K	P					
GGGGGGTCCC	TTAGACTCTC	CTGTGCAGCC	TCTGGATTCA	CTTTCAGTAA	CGCCTGGATG	120													
G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	N	A	W	M
AGTGGGCTCC	GGCAGGCTCC	AGGGAGGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAGGCAA	180													
S	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	R	I	K	S	K
ACTGATGGTG	GGCAACAGA	CTACGGTCCA	CCCGTGAAAG	GCAGATTAC	CATCTCAGC	240													
T	D	G	G	T	T	D	Y	A	A	P	V	K	G	R	F	T	I	S	R
GATGATTCAA	AAACAGCT	GTATCTGCAA	ATGACAGCC	TGAAACCGA	GGACAGCC	300													
D	D	S	K	N	T	L	Y	L	Q	M	N	S	L	K	T	E	D	T	A
GTGTATTACT	GTACACATA	GGGGAGGTT	TACGACCGCG	ATTACGATGG	GGGCTGGGCT	360													
V	Y	Y	C	T	T	Y	G	D	V	Y	D	R	D	Y	D	G	R	W	G
CAGGAACTC	TGGTCAAGCT	CTCTCAGCT	GGAGGGGCT	CAAGGGAGG	TGGCTCTGGC	420													
Q	G	T	L	V	T	V	S	S	G	G	G	S	G	G	G	G	S	G	
GTGGGGGCT	CCGACCTCCA	GATGACCGAG	TCTCAGCTCT	CCCTGTCTGC	ATCTGTAGCA	480													
G	G	G	S	D	I	Q	K	T	Q	S	P	S	S	L	S	A	S	V	G
GACGATCTCA	CCATCACTTC	CGGGGGAGCT	CAGGGGCTTA	GCAATTATTT	AGCCTGGTAT	540													
D	R	V	T	I	T	C	R	A	S	Q	G	I	S	N	Y	L	A	W	Y
CAGGAGAAC	CAGGAGACT	TCTTACGCTC	CTGATCTATG	CTGATCTCAC	TTTGGATCA	600													
Q	Q	K	P	G	K	V	P	K	L	L	I	Y	A	A	S	T	L	Q	S
GGGTCCCAT	CTGGTTCAG	TGGGATGGA	TCTGGAGAG	ATTCACTCT	CACCTCAGC	660													
G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S
AGGTGGGAG	CTGAGATGT	TGGACTTAT	TACTGTCAA	AGTATACAG	TGGCCCTTTC	720													
S	L	Q	P	E	D	V	A	T	Y	Y	C	Q	K	Y	N	S	A	P	F
ATTTCGGAC	CTGGAGCAA	AGTGGATATC	AAACGGGCG	C		761													
T	F	G	P	G	T	K	V	D	I	K									

FIGURE 57

10	20	30	40	50	60	
1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	
GGCCATCCCG	CCATGGCCGA	GGTGCAGCTG	TTGGAGTCTG	GGGAGGCCTT	GGTAAAGCCT	60
	E	V	Q	L	L	E
				S	G	G
					G	L
					V	K
					P	
GGGGGCTCCC	TTAGACTCTC	CTGTGCAGCC	TCTGGATTCA	CTTTCAGTAA	CGCCTGGATG	120
G	G	S	L	R	L	S
		C	A	A	S	G
			F	T	F	S
				N	A	W
					H	
AGCTGGGTCC	GCCAGGCTCC	AGGGAGGGGG	CTGGAGTGGG	TTGGCCGTAT	TAAAGCCAAA	180
S	W	V	R	Q	A	P
		G	K	G	L	E
			W	V	G	R
				I	K	S
					H	
ACTGATGGTG	GGACACAGCA	CTACGCTGCA	CCCGTGAAG	GCAGATTAC	CATCTCAGCA	240
T	D	G	G	T	T	D
		Y	A	A	P	V
			K	G	R	F
				T	I	S
					R	
GATGATTCAA	AAACACGGCT	GTAATCTGCA	ATGACAGGCC	TGAAACCCGA	GGACACAGCC	300
D	D	S	H	N	T	L
		Y	L	Q	M	H
			S	L	K	T
				E	D	T
					A	
GTGTATTACT	GTAACACATA	CGATTAGTGG	GGGTCTTTGG	TGGTCTGGGG	TCAAGGAATC	360
V	Y	Y	C	T	T	Y
		D	W	G	V	L
			V	V	W	G
				Q	G	T
CTGGTCAAGG	TCTCCTCAGG	TGGAGGGGGT	TCAAGGGGAG	GTGCTCTCTG	CGGTGGAGCA	420
L	V	T	V	S	S	G
		G	G	G	S	G
			G	G	G	S
				G	S	G
					G	G
					G	G
TGGACATCC	AGTTGACCC	GTCTCCATCC	TTCTGTCTTG	CATCTGTAGG	AGACAGATCC	480
S	D	I	Q	L	T	Q
		S	P	S	F	L
			S	A	S	V
				G	D	R
					V	
AGCTTCATTT	GCCGGGCGAG	TCAAGGCAAT	AGCAATTAAT	TAGGCTGGTA	TCAAGCAAAA	540
T	I	T	C	R	A	S
		Q	G	I	S	S
			Y	L	A	W
				Y	Q	Q
					H	
CGAGGGAAG	CGCCTAAGCT	CGTATCTAT	GCTGATCC	CTTTGCAAG	TGCGGTCCCA	600
P	G	H	A	P	K	L
		L	I	Y	A	A
			S	T	L	Q
				S	G	V
					F	
TCAAGTTCA	GCGGCATGG	ATCTGACCA	GATTTCACTC	TCAACATCAG	CAAGCTGAG	660
S	R	F	S	G	S	G
		S	G	T	D	F
			T	L	T	I
				S	S	L
				Q		
CTGTAATTT	TTGCACTTA	TTACTGTCAA	CAAGTTAATA	GTTAAGCTTT	CACTTTGGGC	720
P	E	D	F	A	T	Y
		Y	C	Q	Q	L
			N	S	Y	P
				F	T	F
					G	
CTGAGACCA	AAATGATAT	CAAGAGGACC	GCAAGTGC	-		758
P	G	T	H	V	D	I
			H			

FIGURE 58



	CLONES	VHCDR3	
	%Inhibition Activity		
	118:	PFFV	FYRGQDT 54%
?	InsulB:	FVNQHLCGSHLVEAIIY LVCGERGFFYTPKI	
	12H10:	C WYNYA G RG T	42%
Ang?	13-e-4:	VQANDGL G RES	52%
?	13h9:	GGL G REDWL	30%
?	24:	GGRR H RLG	
	InsulinA	GIVEQCCTSIQSLVQ LENYCN	
	11a6:	ENYGNSE	32%
?		GDQELQNY	None
N/A			

FIGURE 59

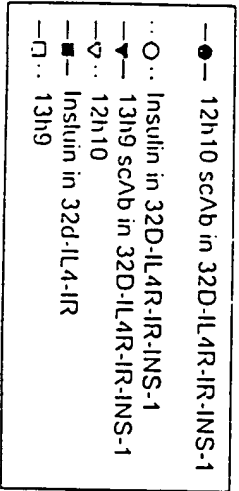
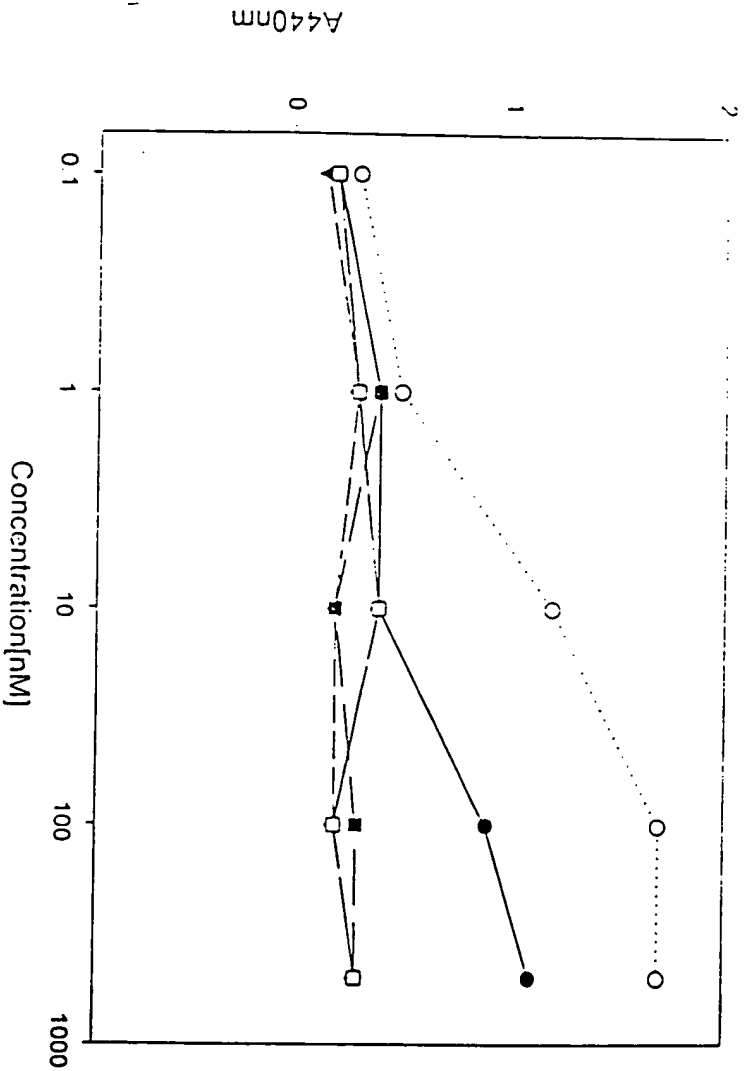


FIGURE 60

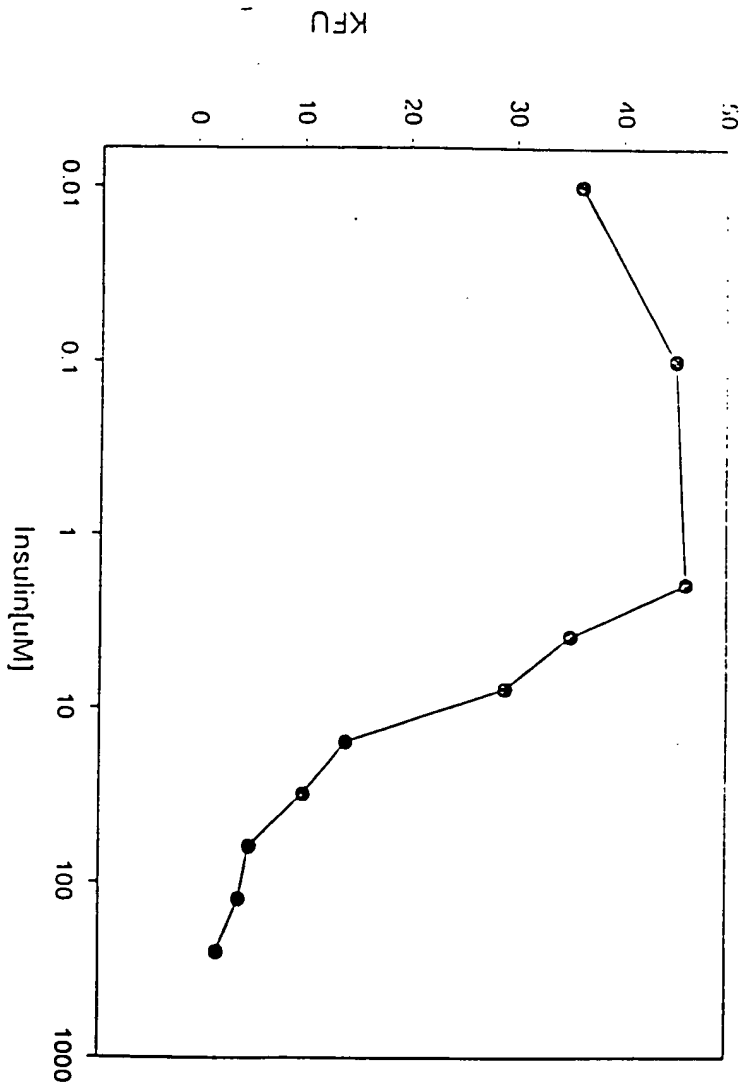


FIGURE 61

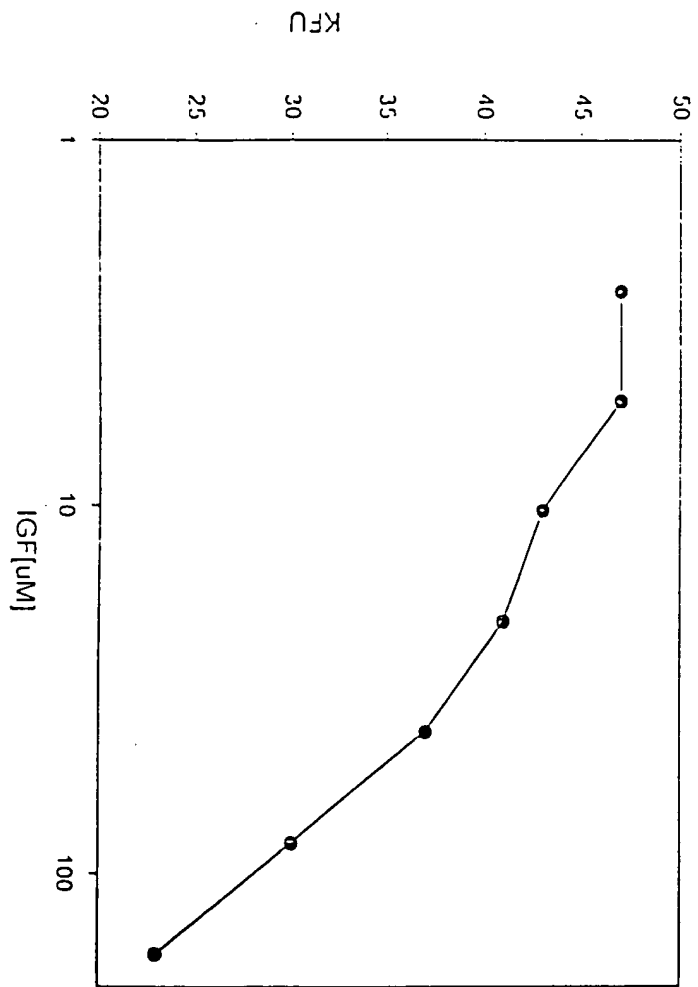


FIGURE 62

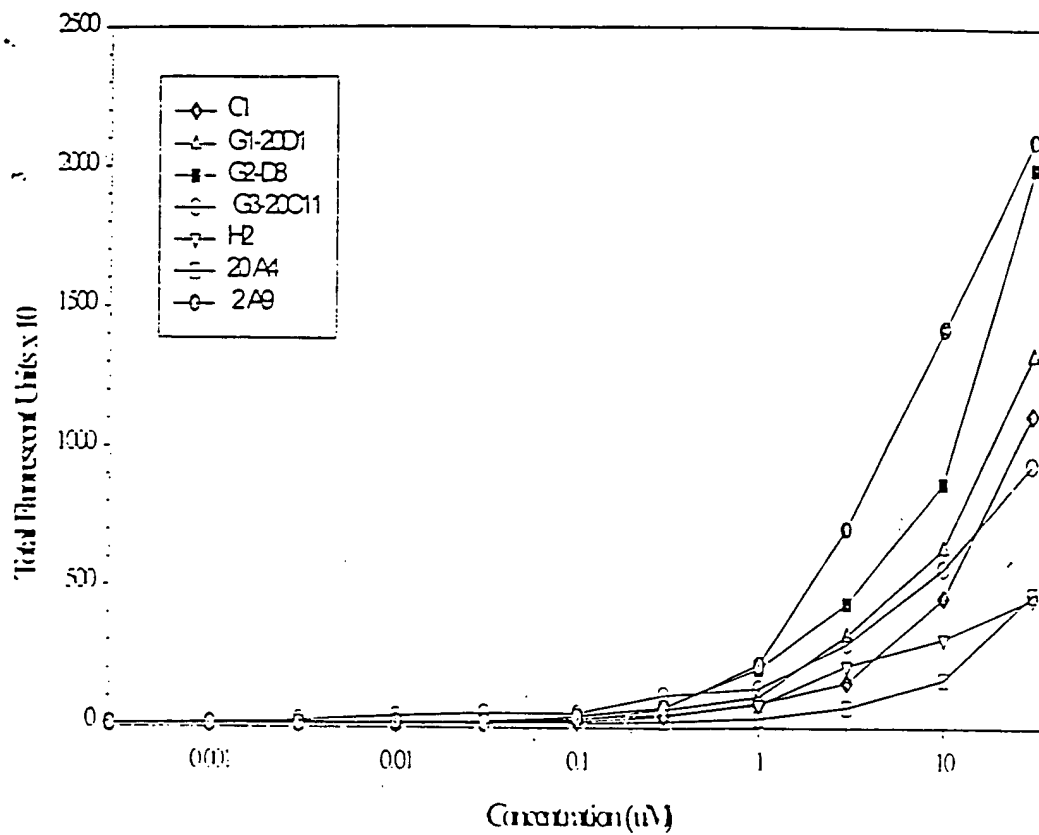


FIGURE 63

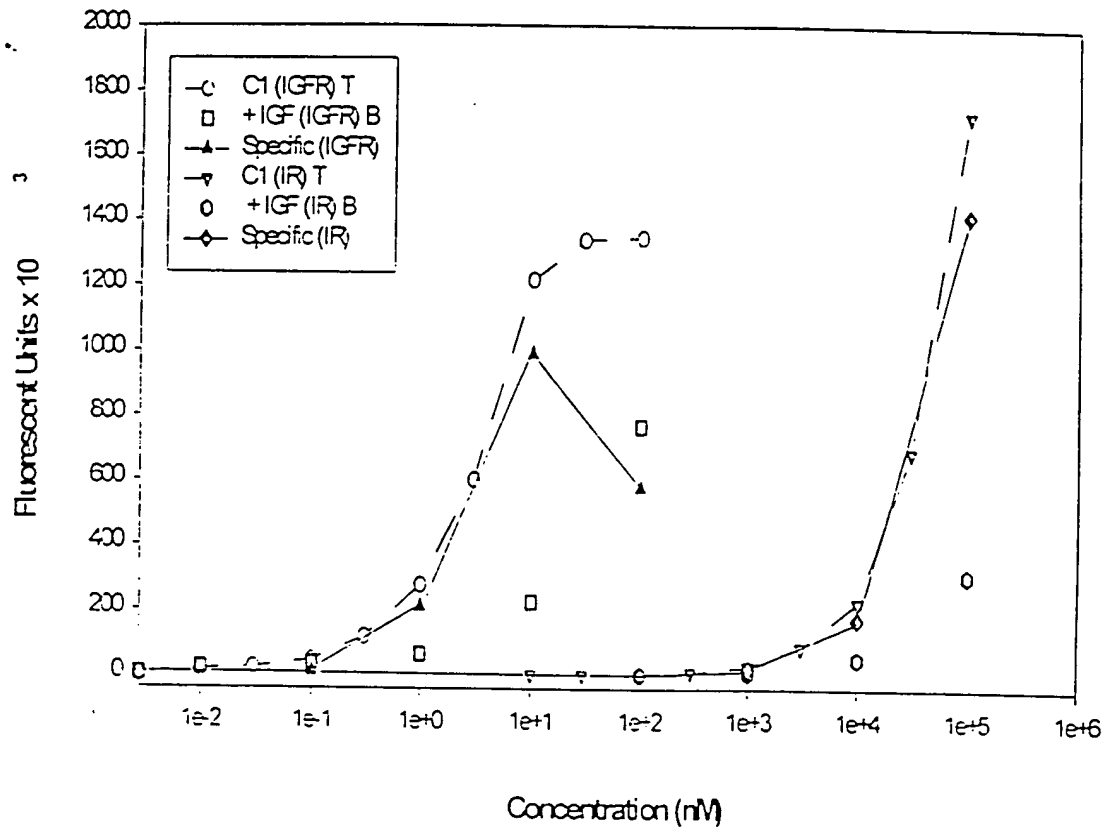


FIGURE 64

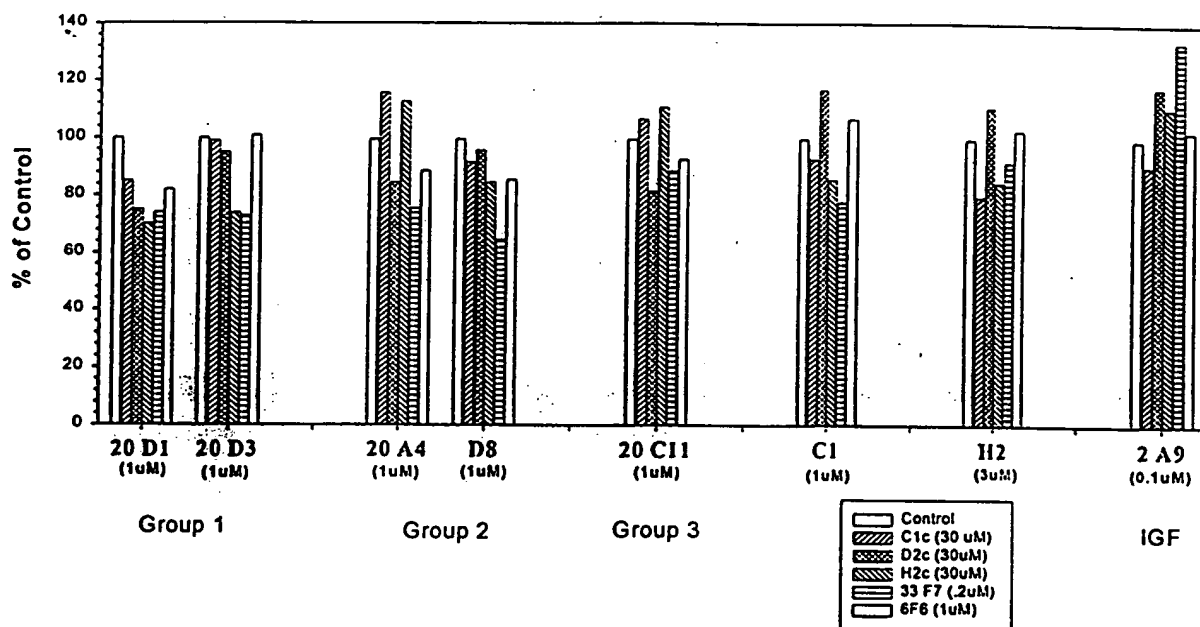


FIGURE 65

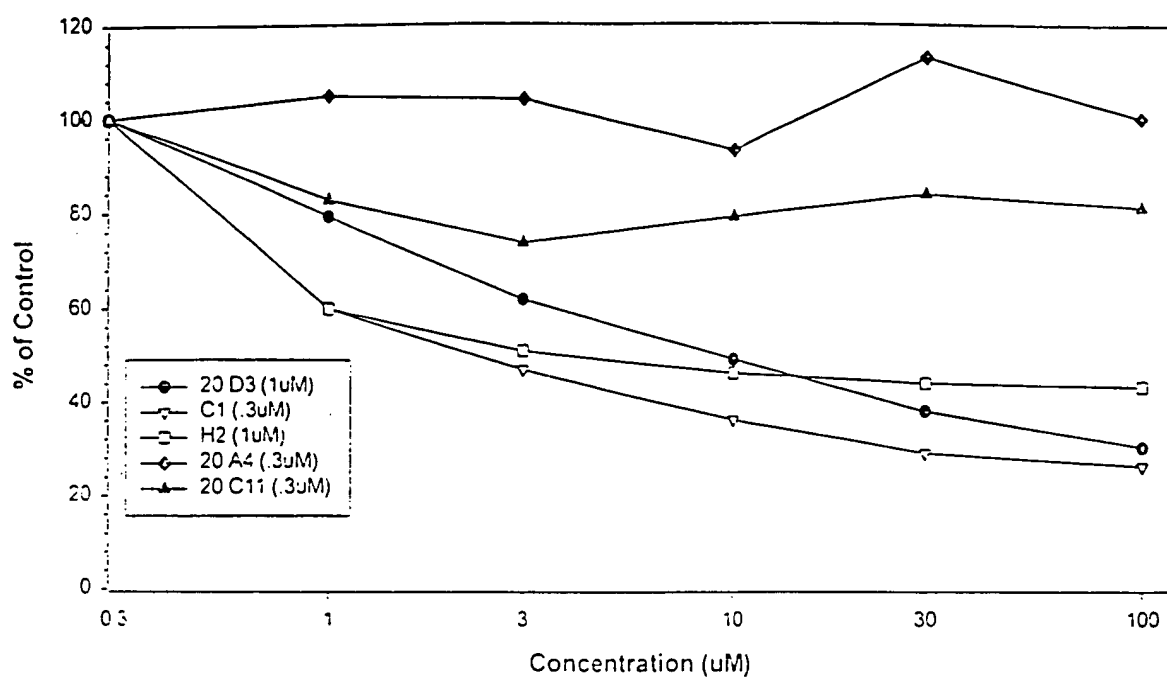


FIGURE 66

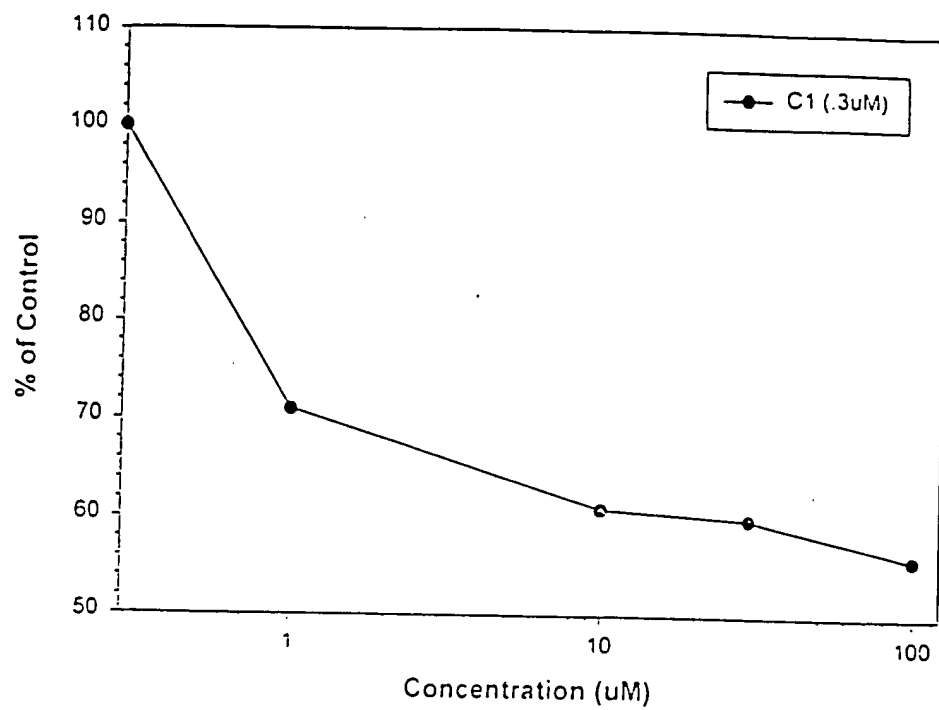


FIGURE 67

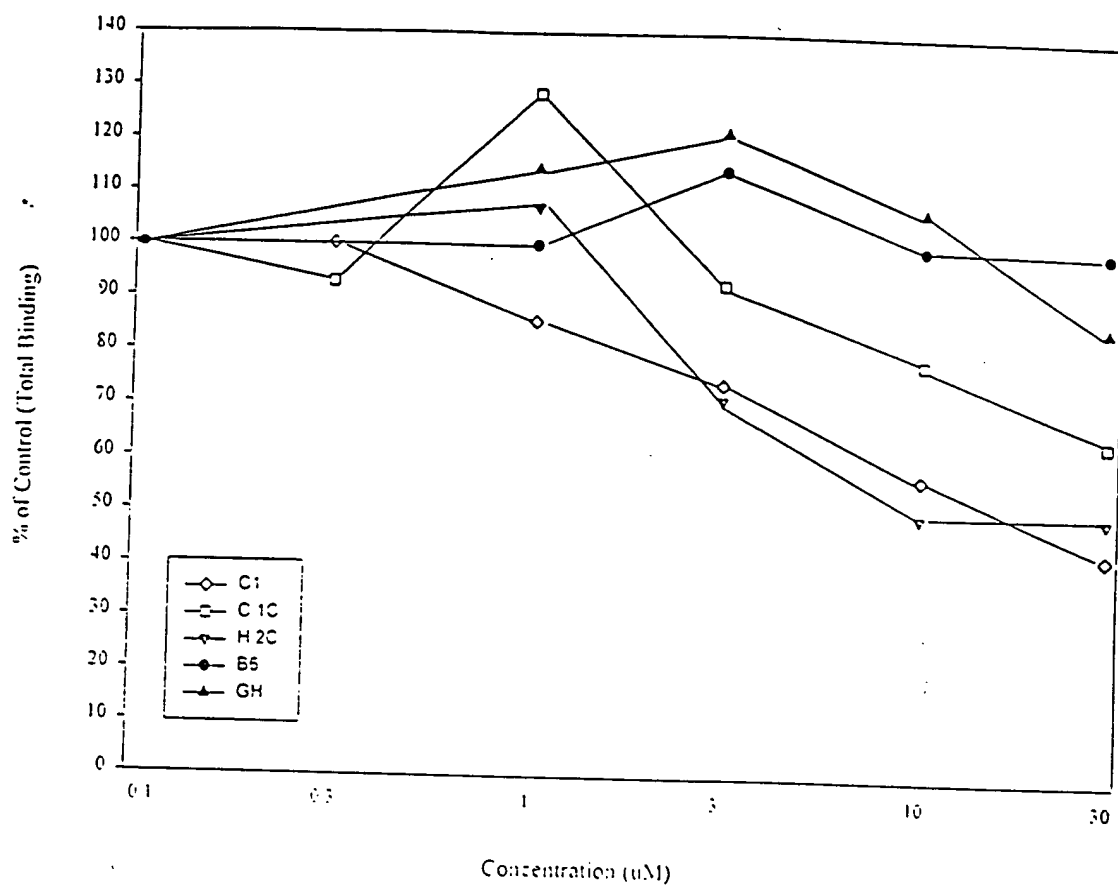


FIGURE 68

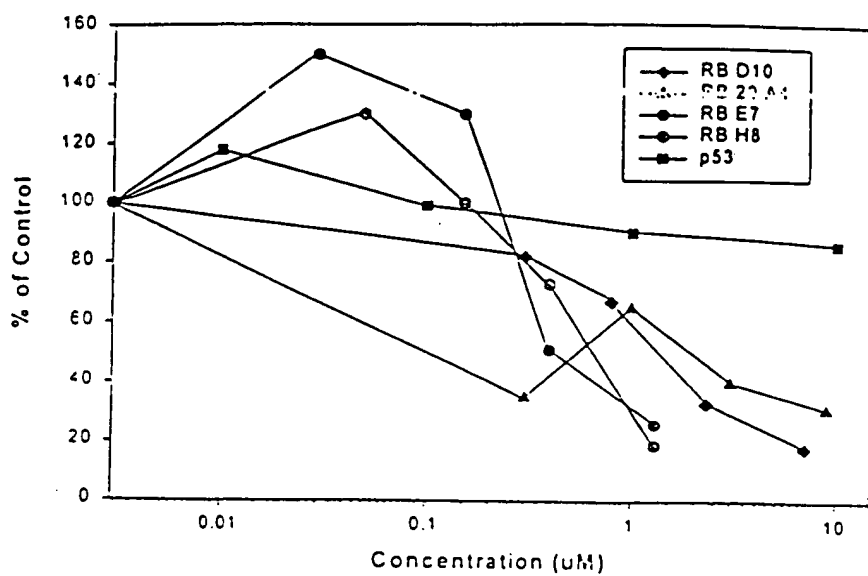


FIGURE 69

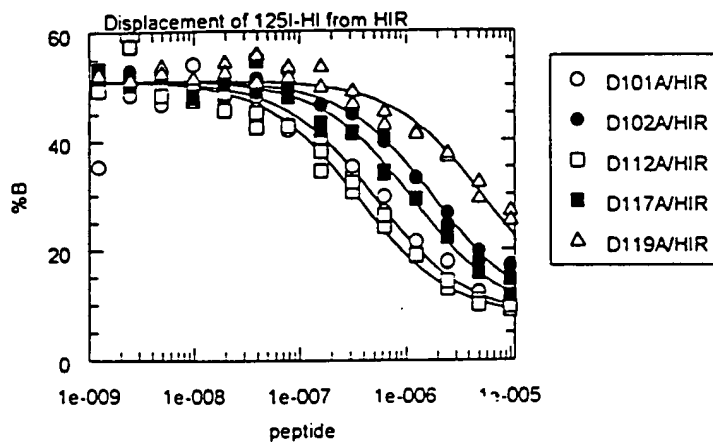


FIGURE 70A D990114A

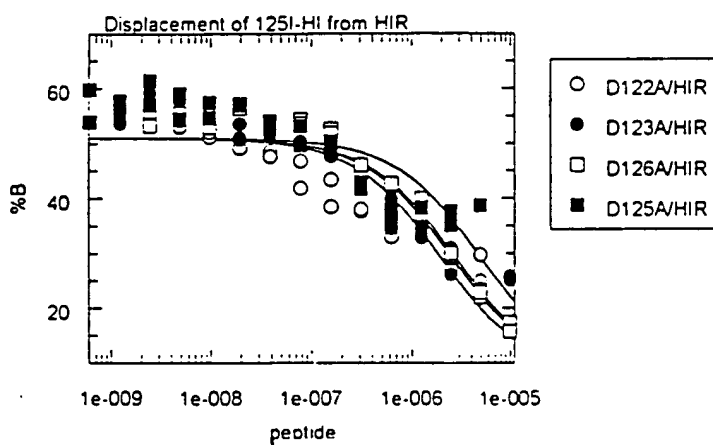


FIGURE 70B D990118A

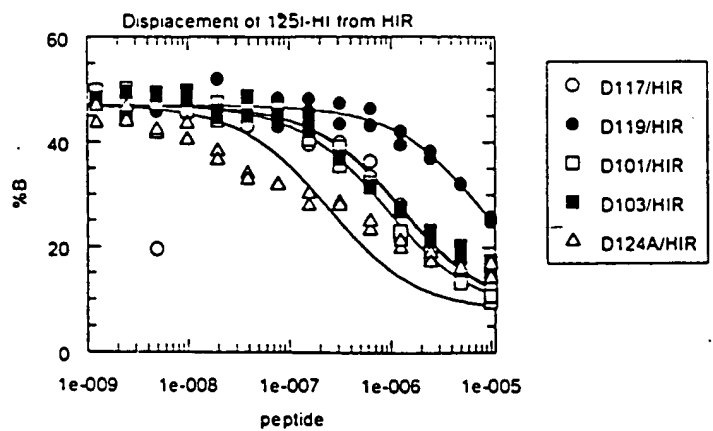


FIGURE 70C D990126A

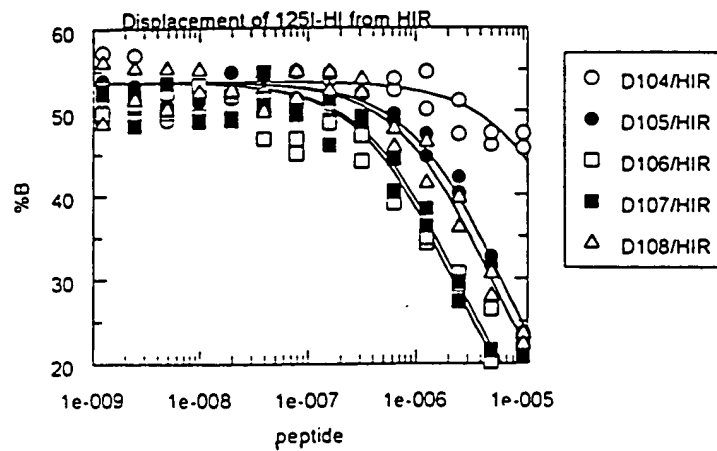


FIGURE 70D

D990129A

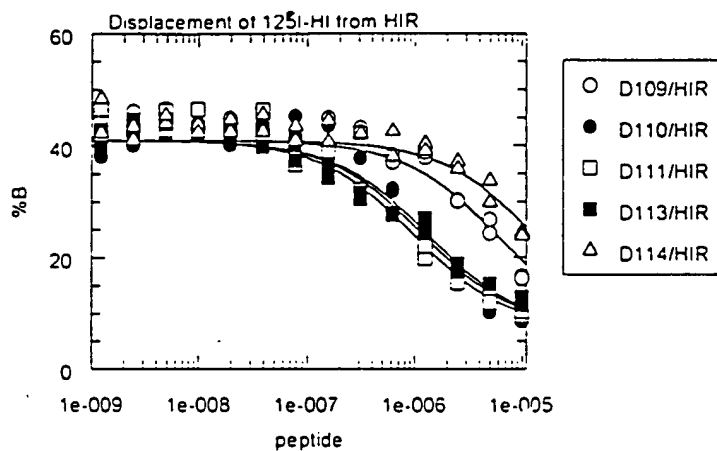


FIGURE 70E

D990202A

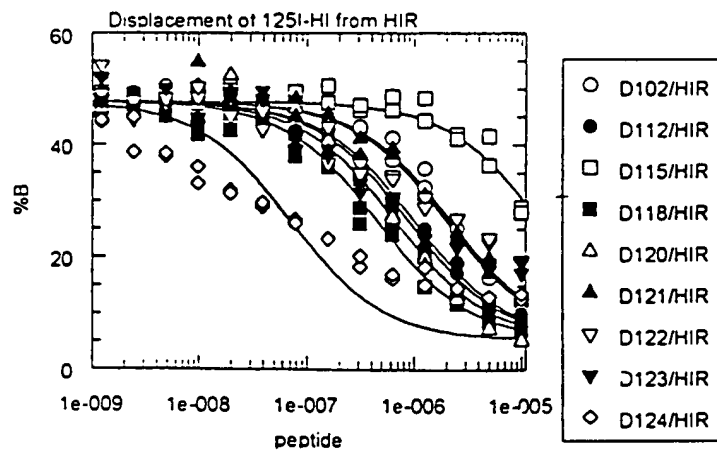


FIGURE 70F

D990205A

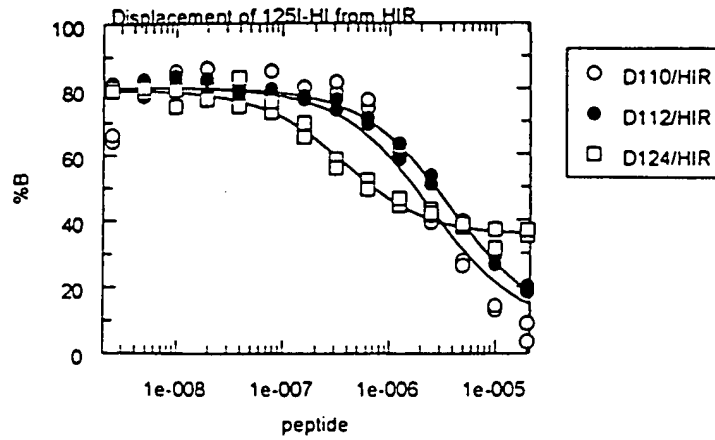


FIGURE 70G

D990217A

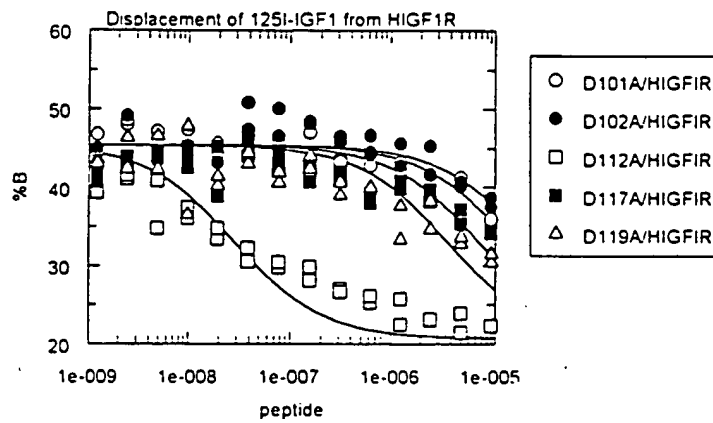


FIGURE 70H

D990114A

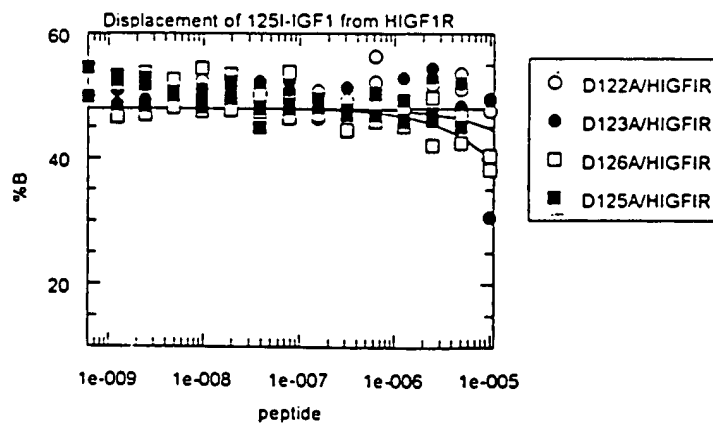


FIGURE 70I

D990118A



FIGURE 70L

D990202A

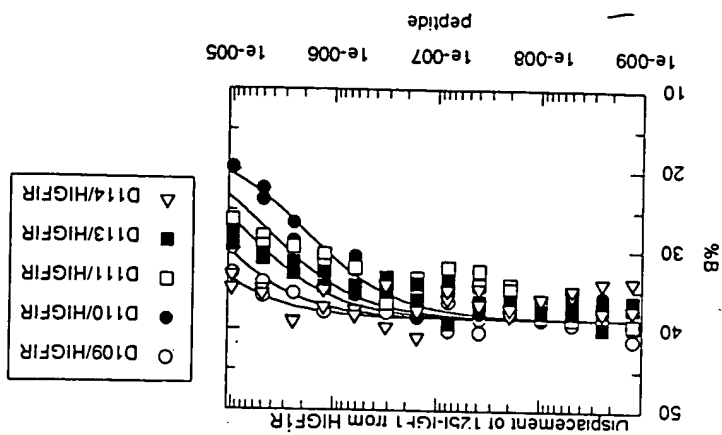


FIGURE 70K

D990129A

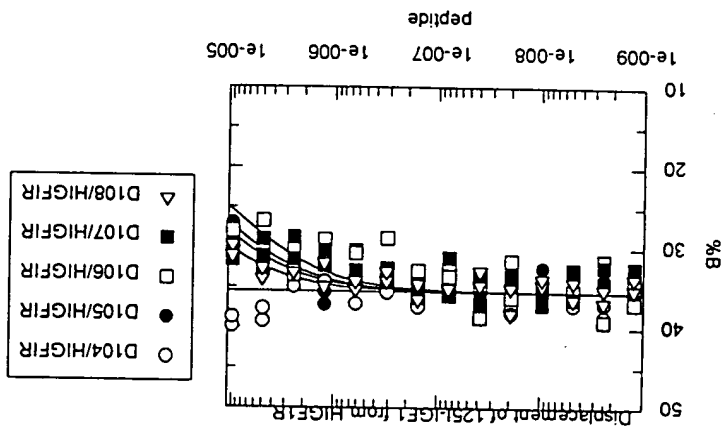
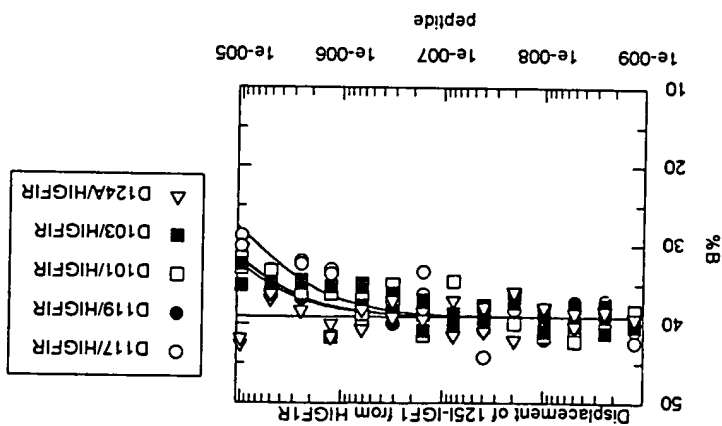


FIGURE 70J

D990126A



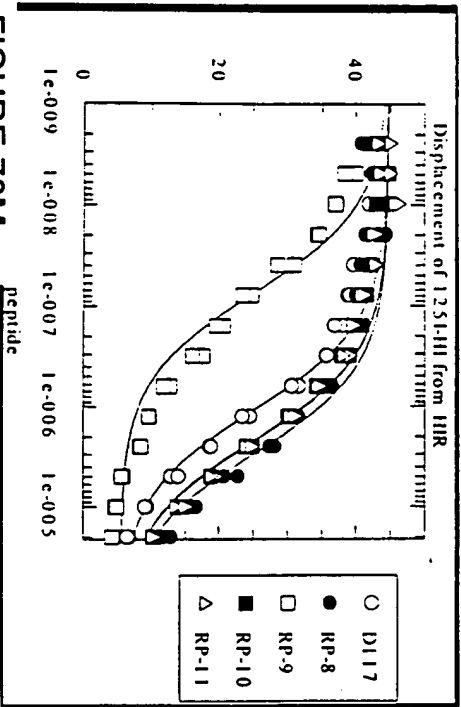


FIGURE 70M

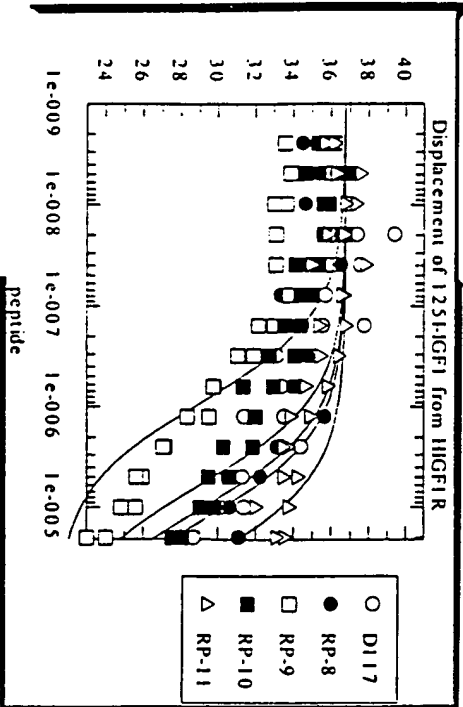


FIGURE 70N

FIGURE 71A

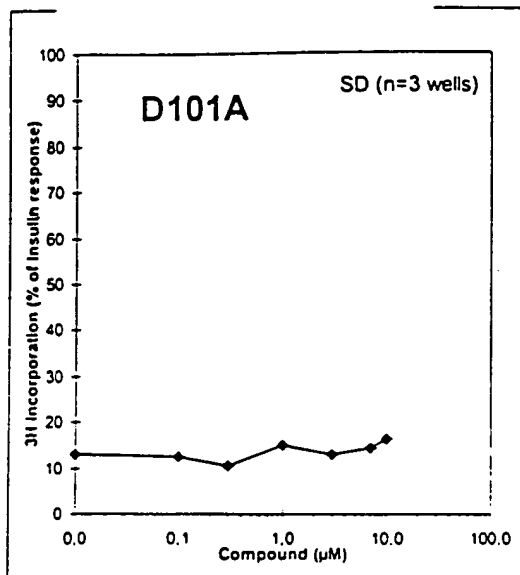


FIGURE 71B

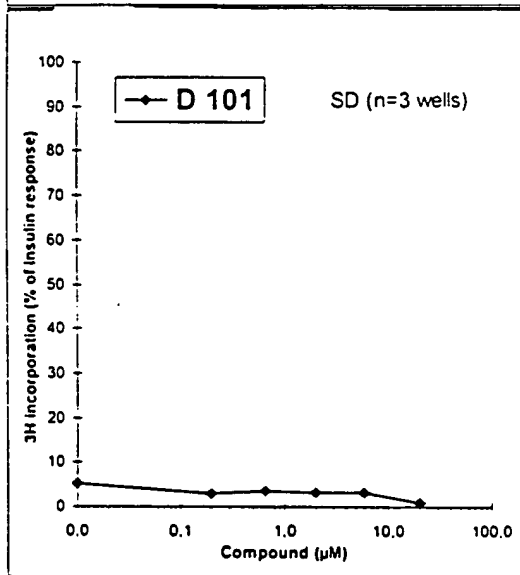
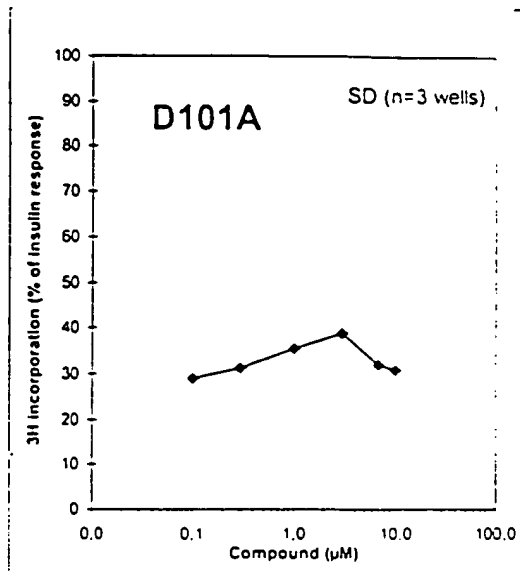


FIGURE 71C

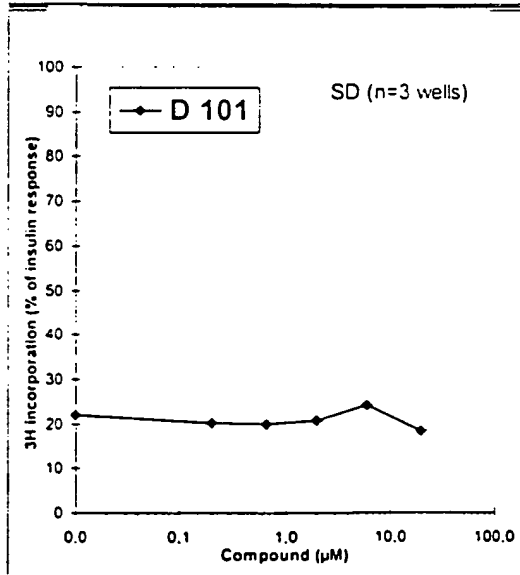


FIGURE 71D



FIGURE 71E

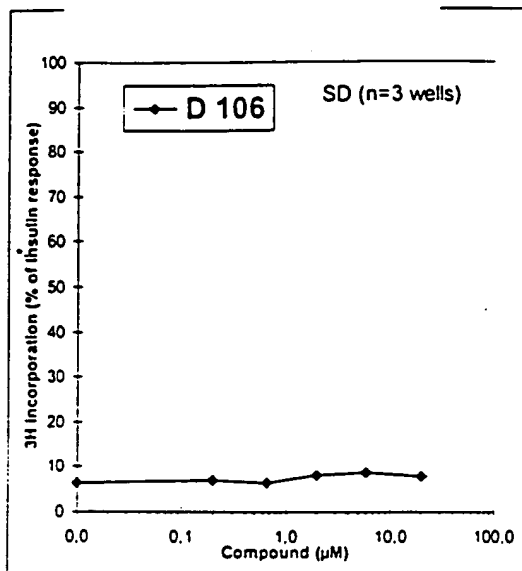


FIGURE 71F

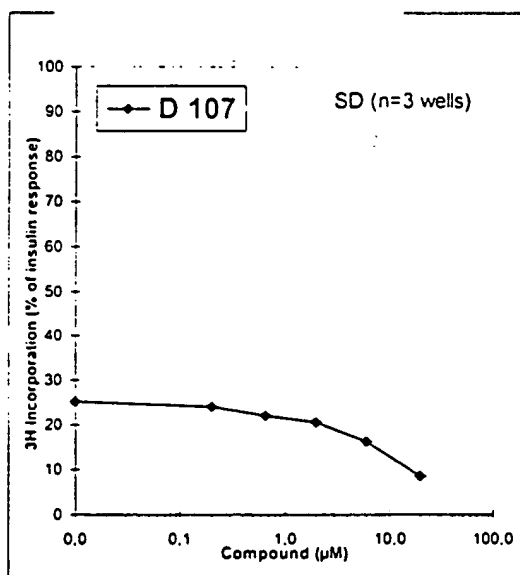
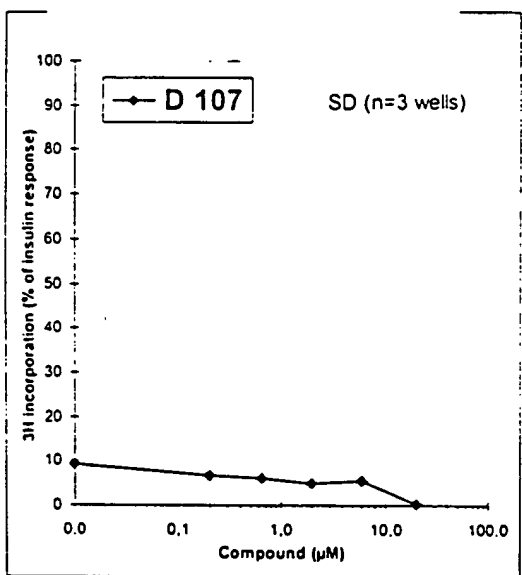
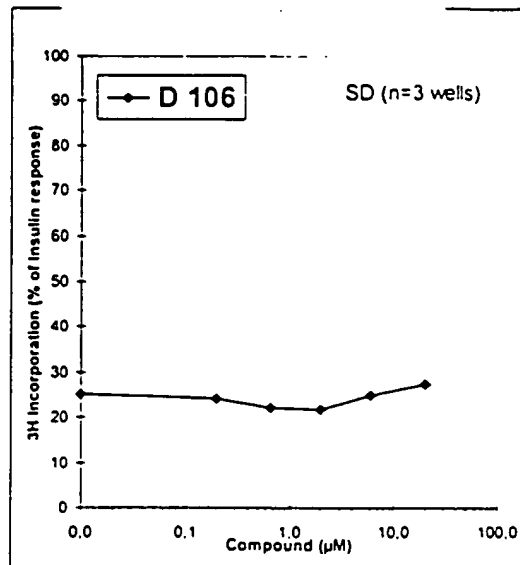


FIGURE 71G

FIGURE 71H



FIGURE 71I

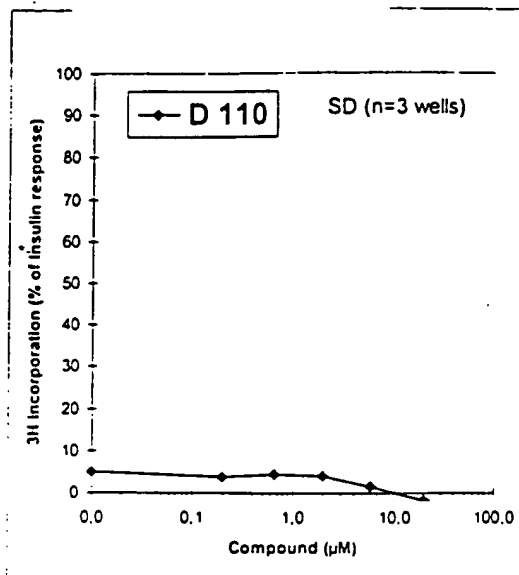


FIGURE 71J

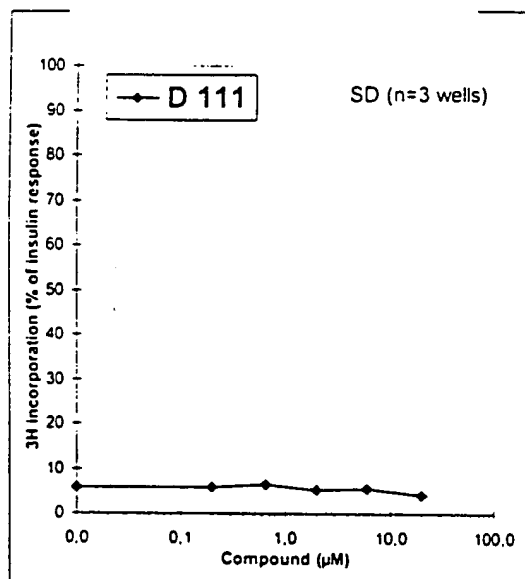
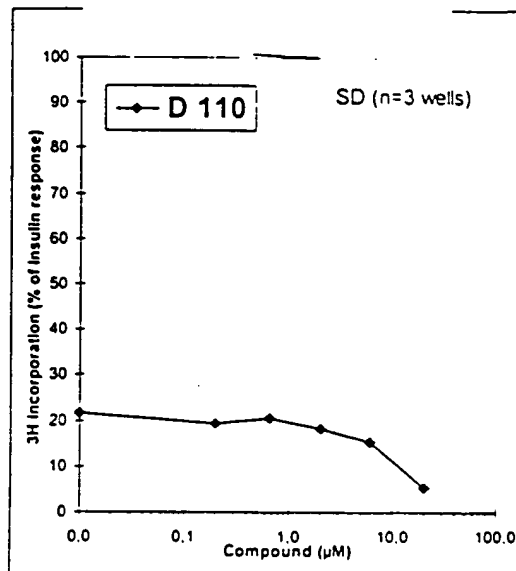


FIGURE 71K

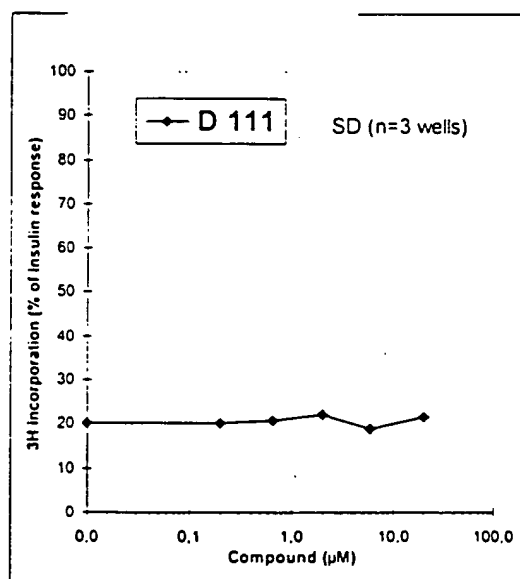


FIGURE 71L



FIGURE 71M

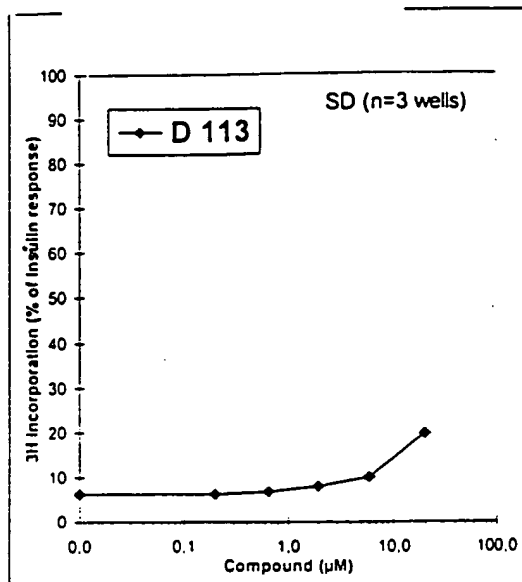


FIGURE 71N

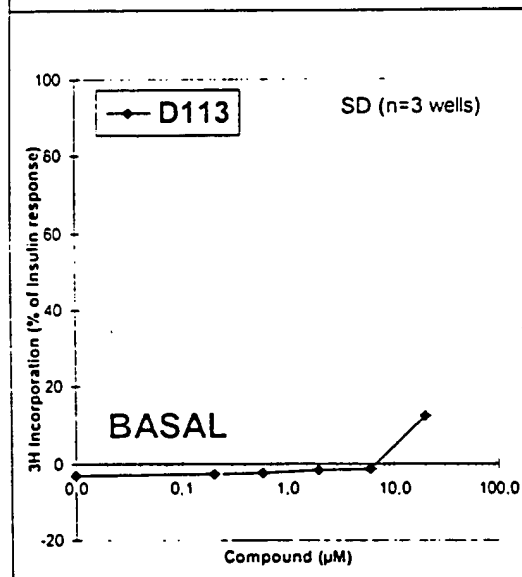
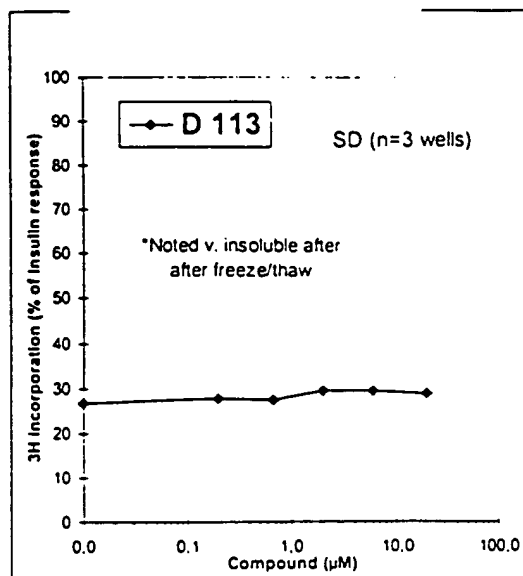


FIGURE 71O

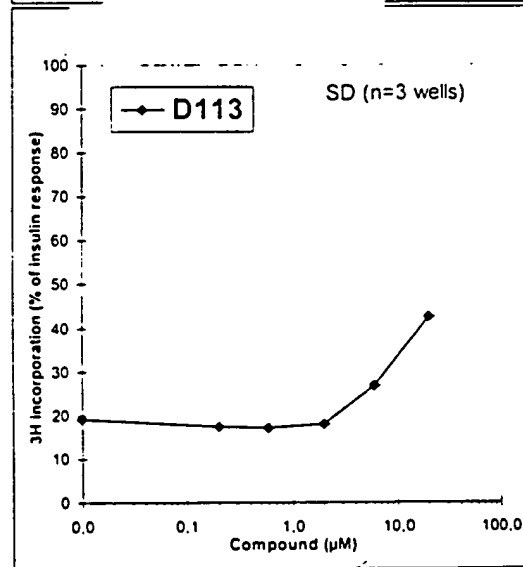


FIGURE 71P



FIGURE 71Q

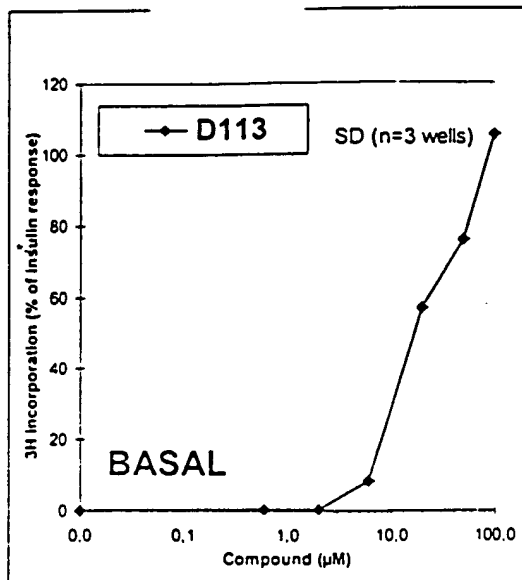


FIGURE 71R

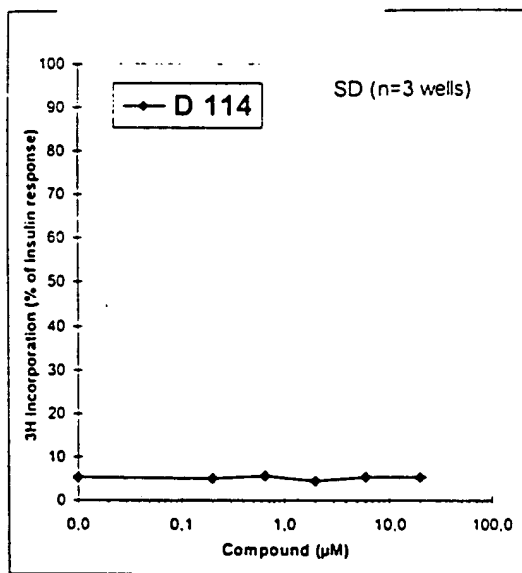
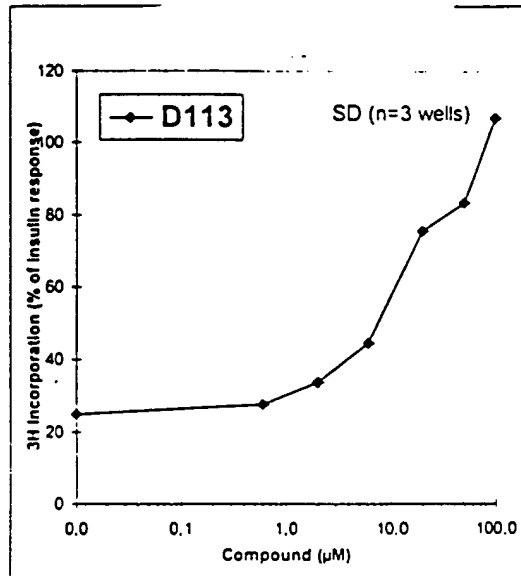


FIGURE 71S

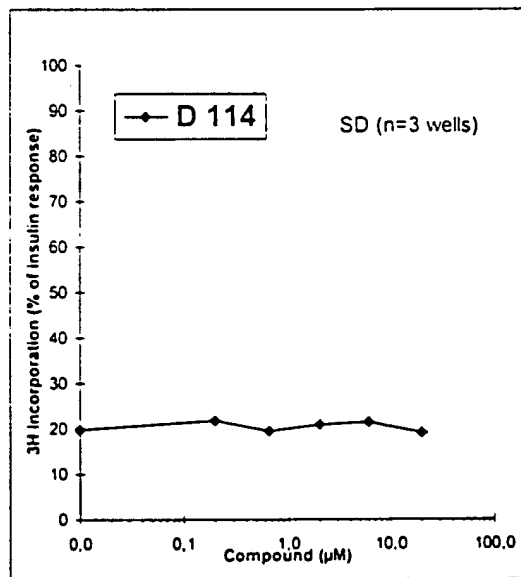


FIGURE 71T



FIGURE 71U

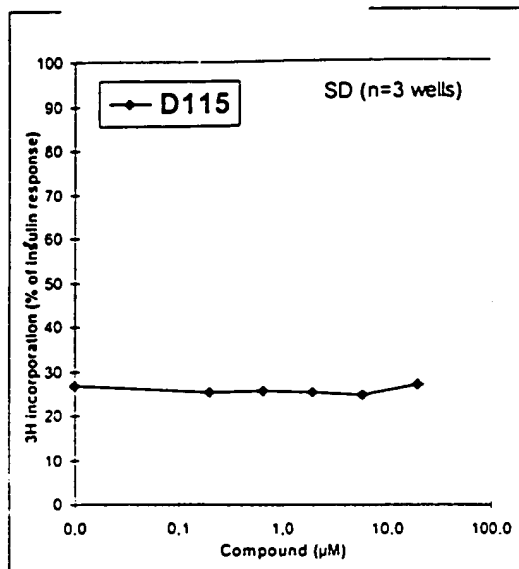


FIGURE 71V

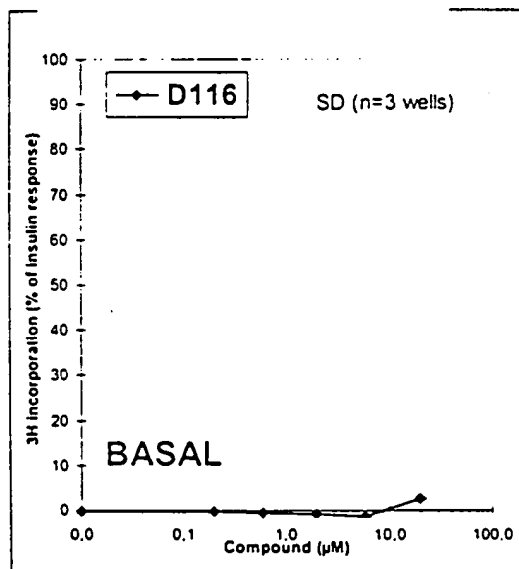
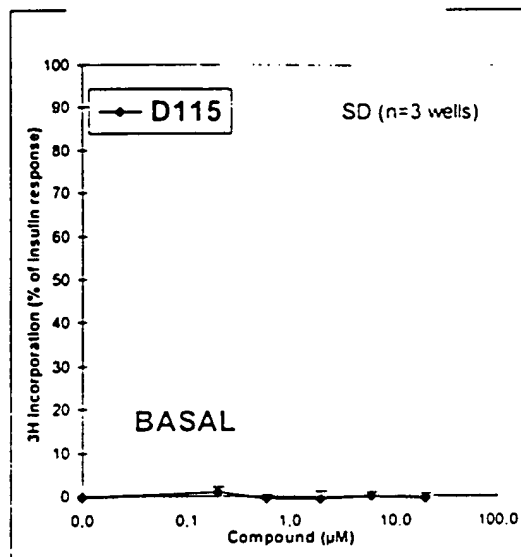


FIGURE 71W

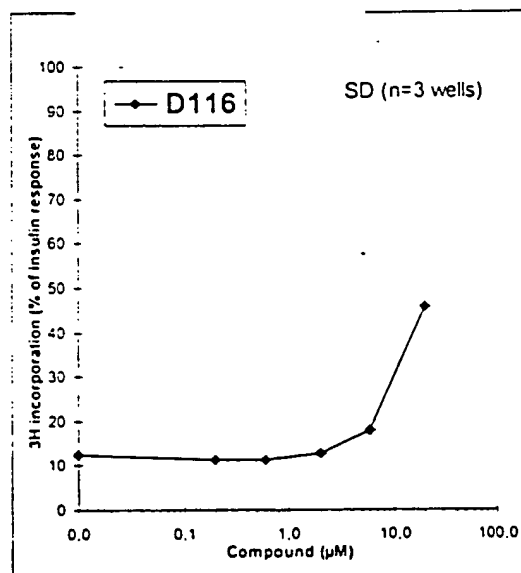


FIGURE 71X



FIGURE 71Y

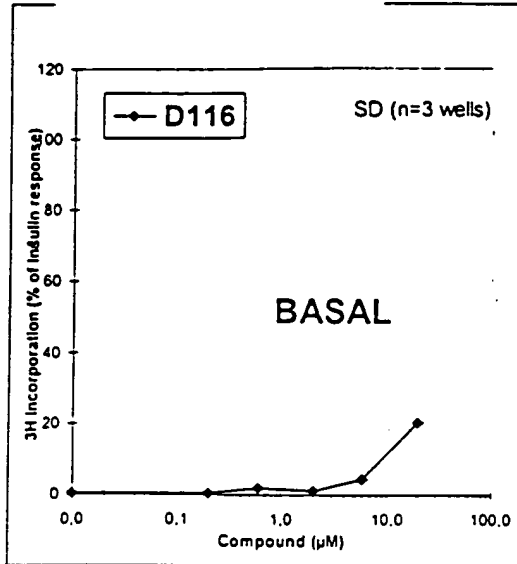


FIGURE 71Z

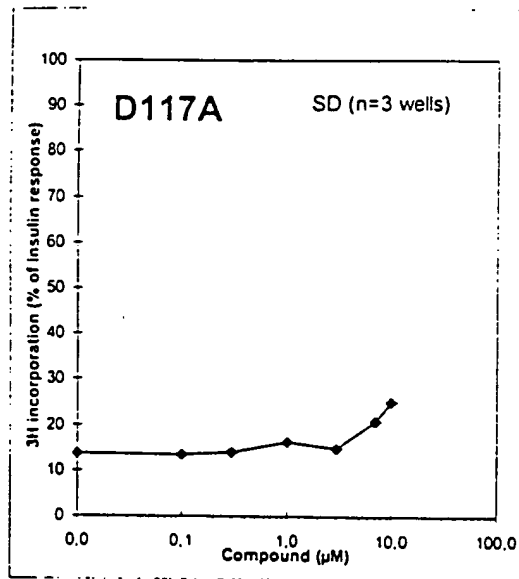
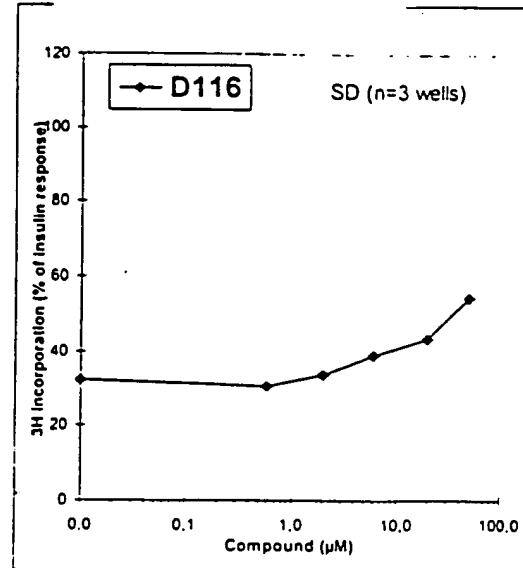


FIGURE 71A2

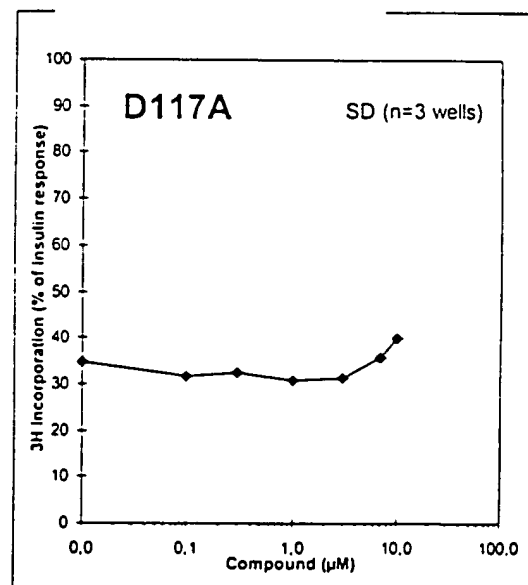


FIGURE 71B2



FIGURE 71C2

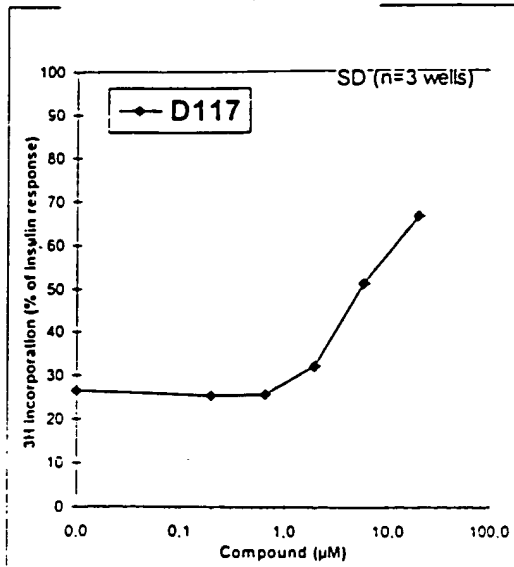


FIGURE 71D2

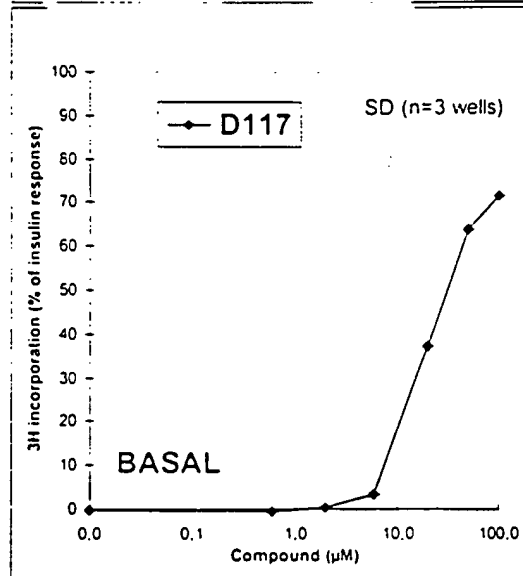
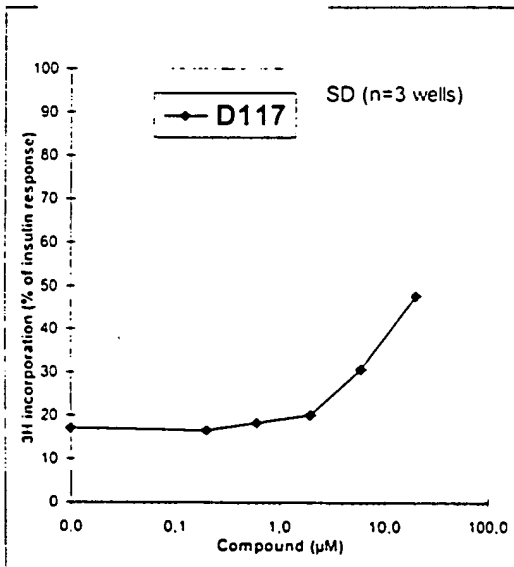
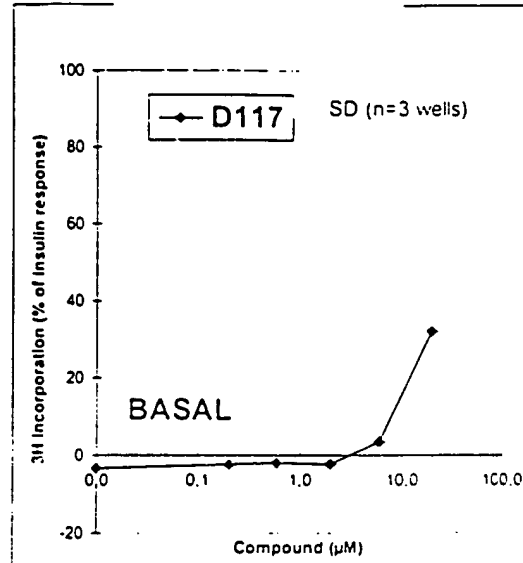


FIGURE 71E2

FIGURE 71F2



FIGURE 71G2

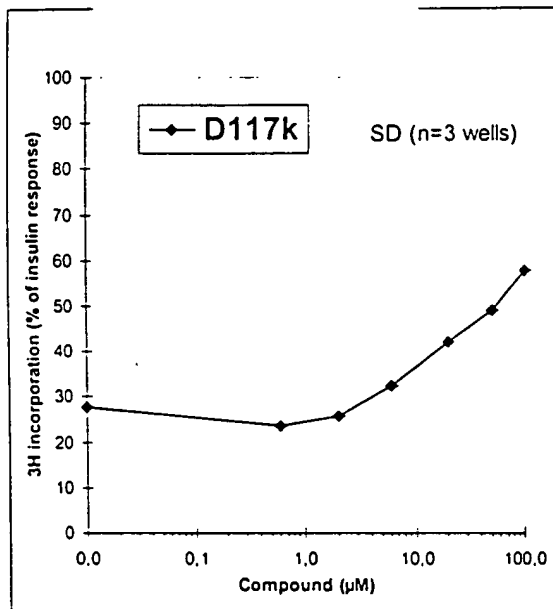
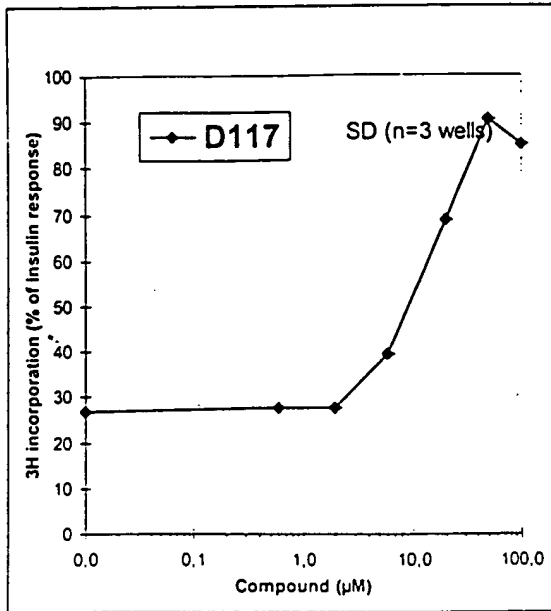


FIGURE 71H2

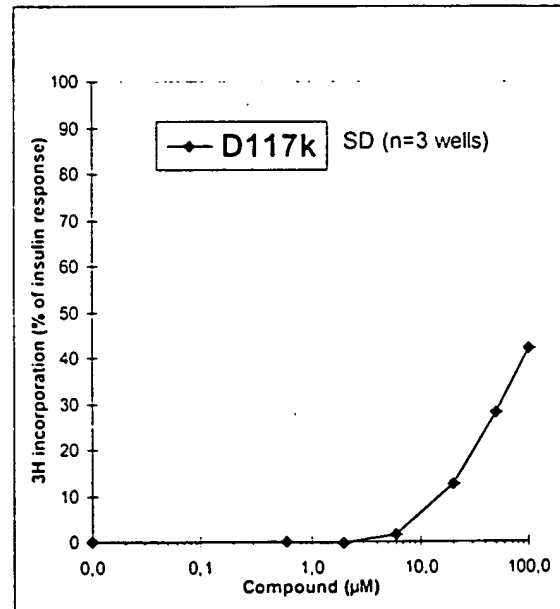


FIGURE 71I2



FIGURE 71J2

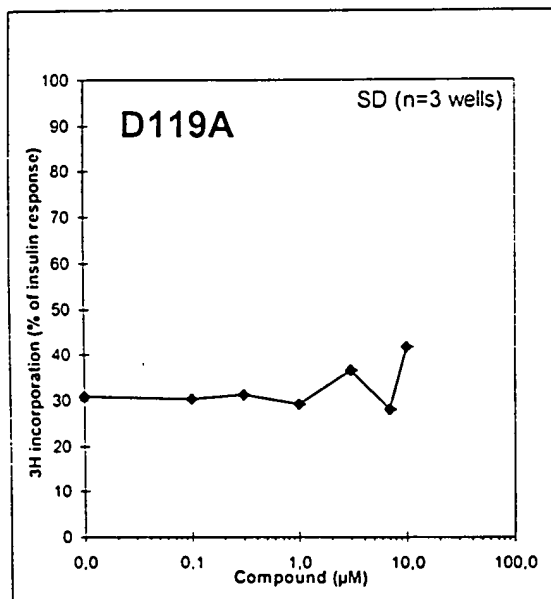
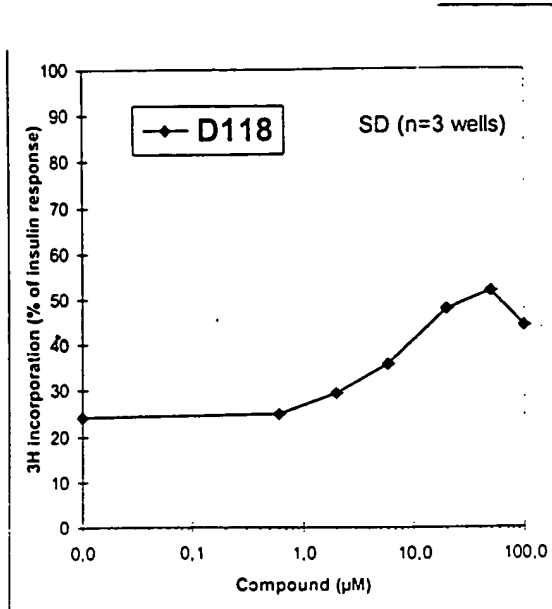


FIGURE 71K2

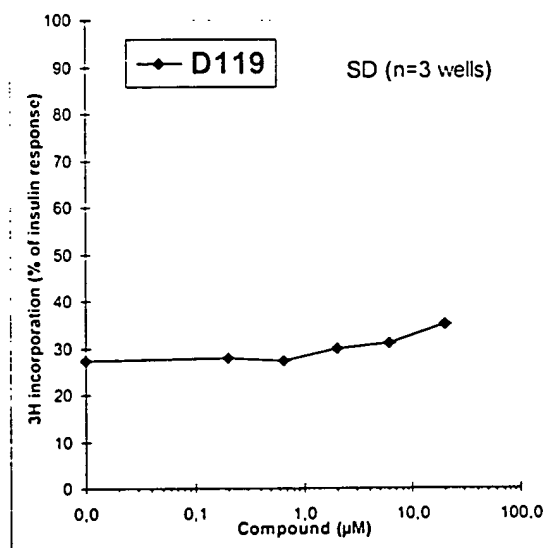


FIGURE 71L2



FIGURE 71M2

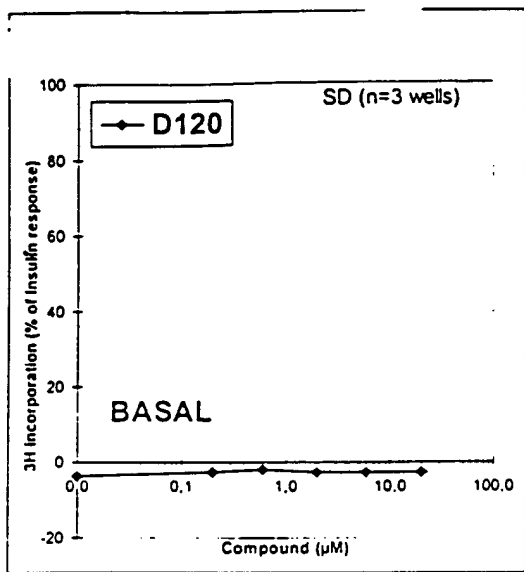


FIGURE 71N2

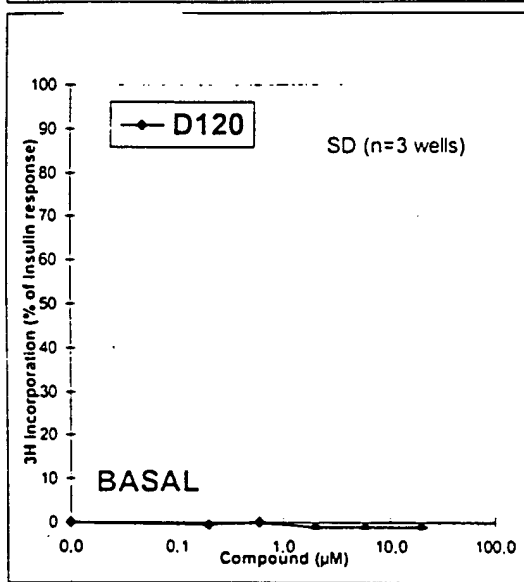
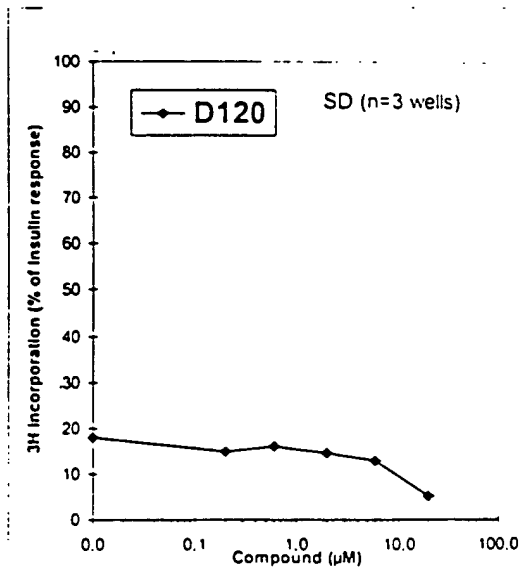


FIGURE 71O2

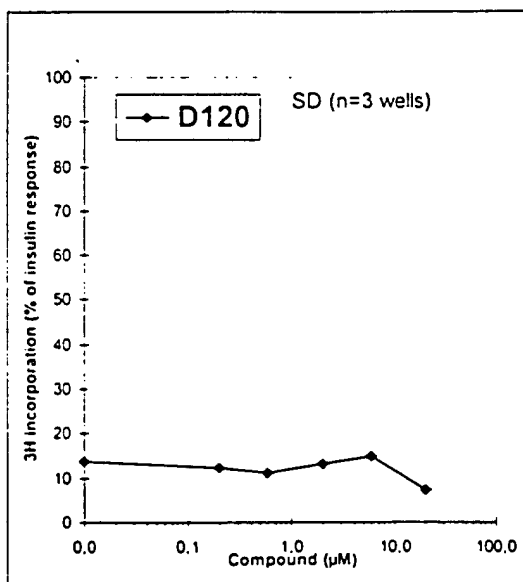


FIGURE 71P2



FIGURE 71Q2

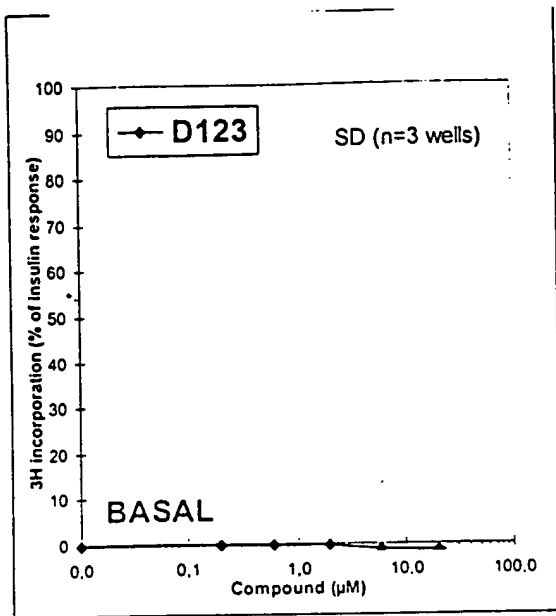


FIGURE 71R2

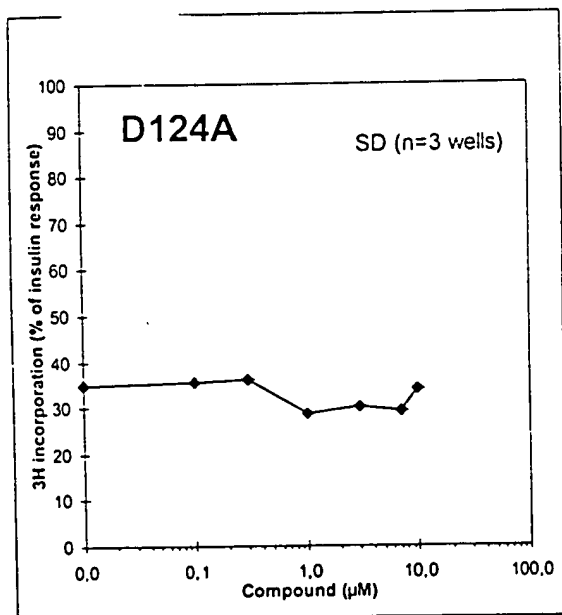
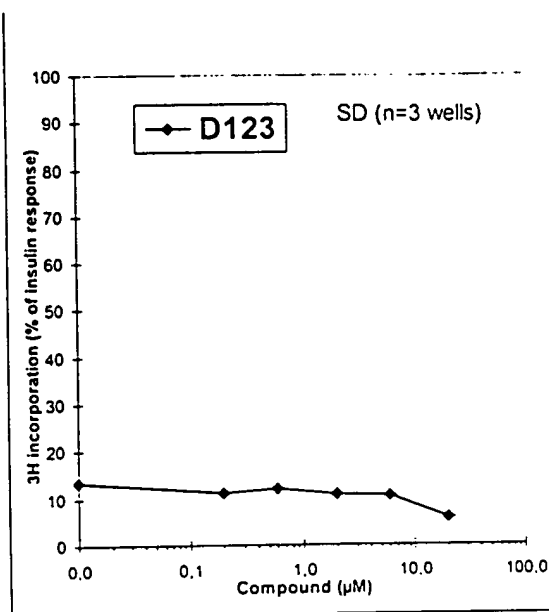


FIGURE 71S2



FIGURE 71T2

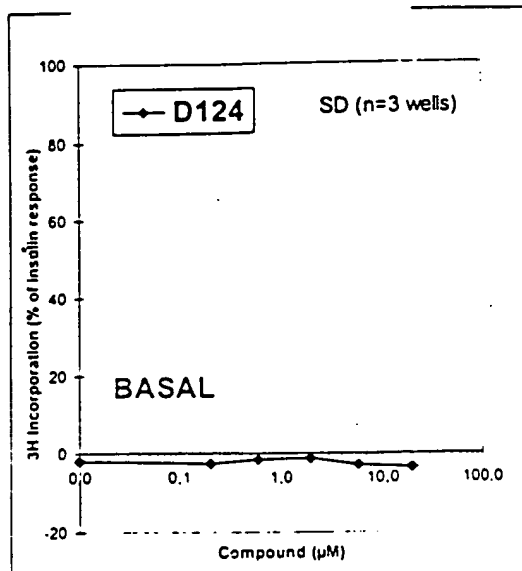


FIGURE 71U2

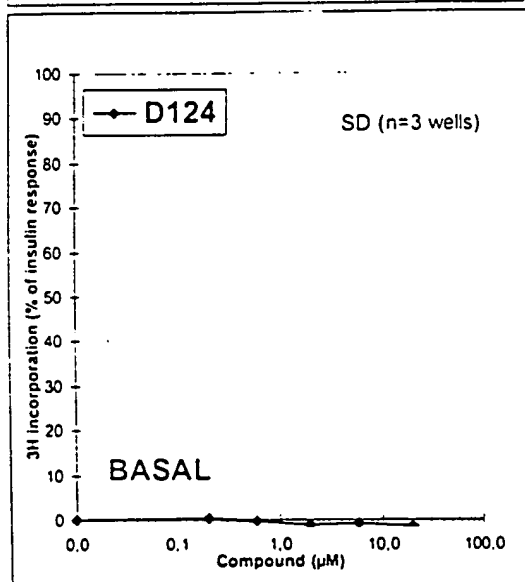
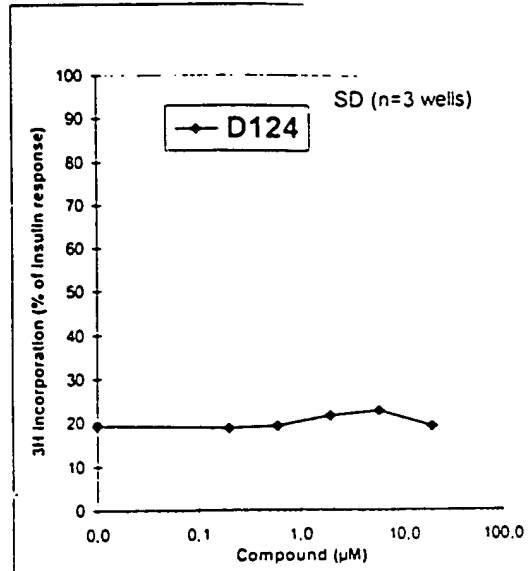


FIGURE 71V2

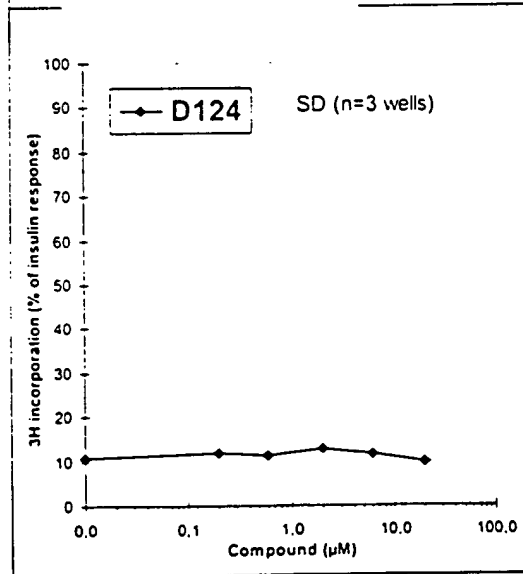


FIGURE 71W2



FIGURE 71X2

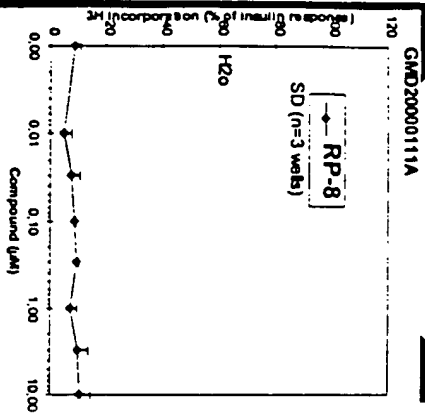
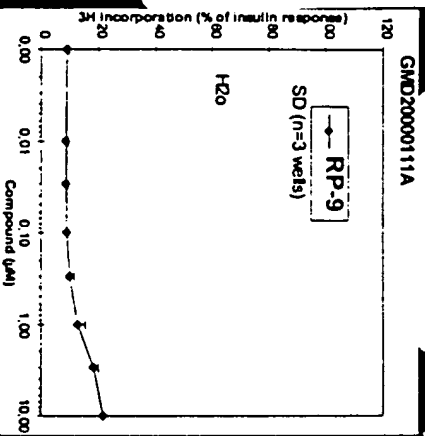


FIGURE 71Y2



GMD20000111A GM

GMD20000111A

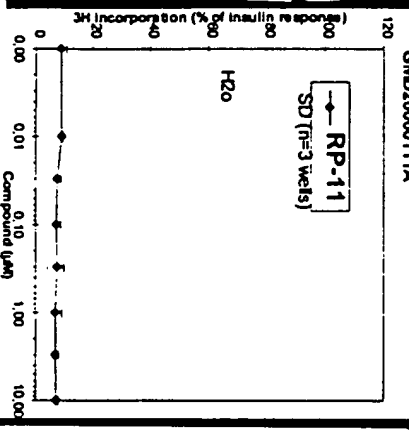
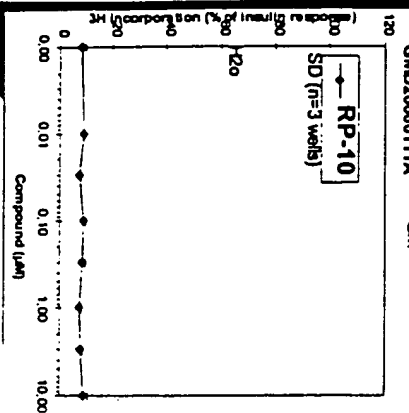


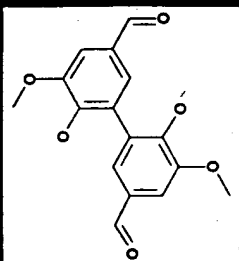
FIGURE 71Z2

FIGURE 71A3

S291: Dimer of S204 with linker 9

S204 = Lig-GGGFHENFYDWFVRQVSKK

Linker 9 =



HIR binding = $1.2 \cdot 10^{-6}$

FEC:

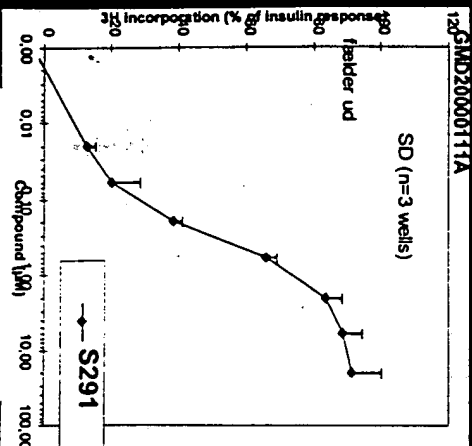


FIGURE 71B3





FIGURE 72A

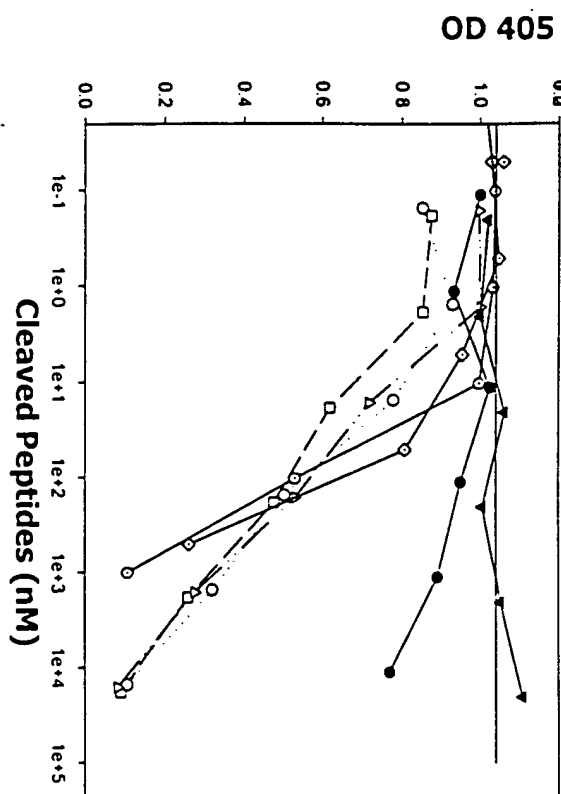
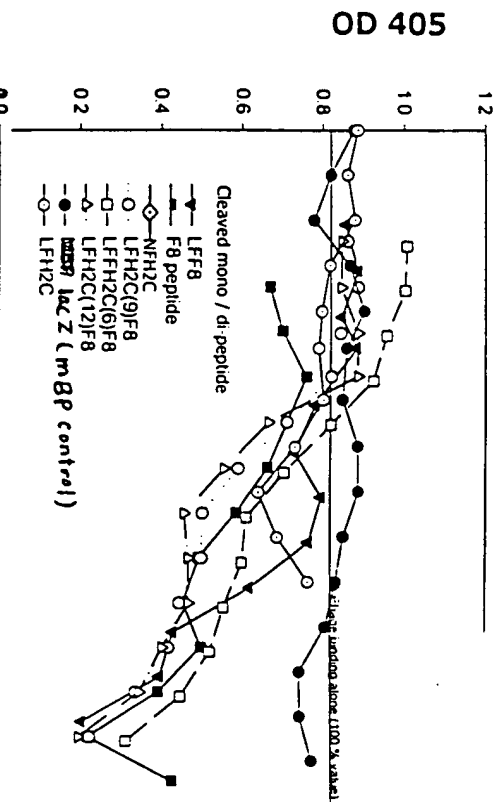


FIGURE 72B

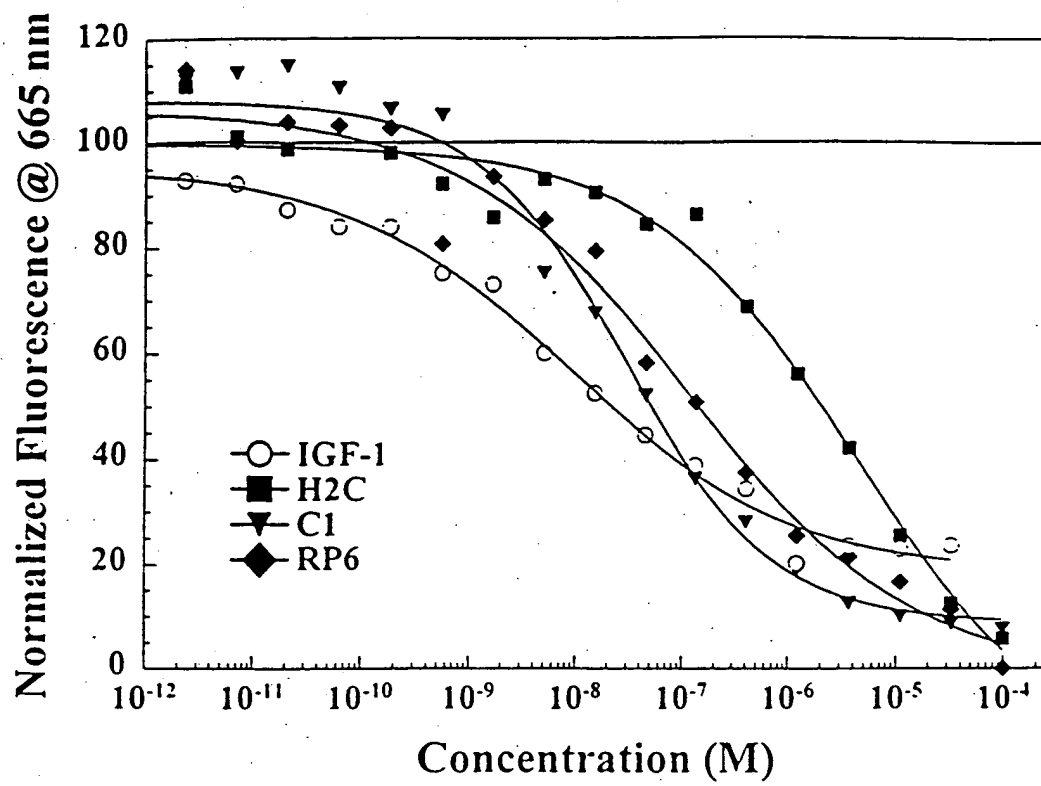


FIGURE 73



FIGURE 74

